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US-08-446-915-2.rsp

N

(MT)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 10 07:03:26 1996; MasPar time 11.71 Seconds 607.114 Million cell updates/sec

Tabular output not generated.

>US-08-446-915-2 (1-409) from US08446915.pep 2945

Description: Perfect Score:

Sequence: 1 MASSSAPDENEFQFGCPPAP......KHAYVKDDTMF1KCIVDTSA 409

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

49340 seqs, 17385503 residues

Database:

swiss-prot32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Statistics: Mean 49.616; Variance 101.312; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ID	Description	Pred. No.
1	2945	100.0	409	œ	TRF1 MOUSE	TNF RECEPTOR ASSOCIAT	0.00e+00
2	972	33.0	501	œ	TRF2 MOUSE	TNF RECEPTOR ASSOCIAT	3.50e-163
w	148	5.0	760	5	MEPA MOUSE	MEPRIN A ALPHA-SUBUNI	7.90e-07
4	127	4.3	1048	٦	SBCC ECOLI	EXONUCLEASE SBCC.	7.06e-04
5	120	4.1	2291	7	SPCB DROME	SPECTRIN BETA CHAIN.	6.00e-03
5	115	3.9	1319	w	DY15 DROME	150 KD DYNEIN-ASSOCIA	2.65e-02
7	112	3.8	493	4	INVO SAGOE	INVOLUCRIN.	6.32e-02
<b>∞</b>	112	3.8	870	6	POL JSRV	POL POLYPROTEIN (REVE	6.32e-02
9	113	3.8	1427	-1	REST HUMAN	RESTIN (CYTOPLASMIC L	4.74e-02
10	109	3.7	544	4	INVO AOTTR	INVOLUCRIN.	1.49e-01
=	106	3.6	668	Ç	MEPB RAT	MEPRIN A BETA-SUBUNIT	3.44e-01
12	105	3.6	776	_	ARCB ECOLI	AEROBIC RESPIRATION C	4.53e-01
13	107	3.6	2663	2	CENE_HUMAN	CENTROMERIC PROTEIN E	2.61e-01

В

1 masssapdenefqfgcppapcqdpseprvlcctaclsenlrddedricpkcradnlhpvs 60

# ALI GNMENTS

	SC	<b>~</b>	ΡE	S	c	c	2	2	R	25	æ	₽	8	8	9	DE	2	2	9	A(	H	æ
Query Match 100.0%; Score 2945; DB 8; Length 409; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps	SQ SEQUENCE 409 AA; 45464 MW; 857796 CN;	KW COILED COIL.	DR EMBL; L35302; L35302.	CC -!- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.	CC -!- SUBCELLULAR LOCATION; CYTOPLASMIC.	CC OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).	CC TUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN	RL CELL /8:681-692(1994).	RA ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;	RX MEDLINE; 94349371.	RP SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND 390-402.	RN [1]	OC EUTHERIA; RODENTIA.	OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	OS MUS MUSCULUS (MOUSE).	DE TNF RECEPTOR ASSOCIATED FACTOR 1 (TRAF1).	DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)	DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)	DT 01-FEB-1995 (REL. 31, CREATED)	AC P39428;	ID TRF1_MOUSE STANDARD; PRT; 409 AA.	RESULT 1
DB 8; Length 409; )0e+00; ses 0; Indels				F2.		CEPTOR (TNF-R2)	D WITH THE CYTO		D.V.;		.35 AND 390-402.			TETRAPODA; MAMI			ATE)	H			AA.	
09;						•	PLASMI							ALIA;								
Gaps 0;							C DOMAIN															

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RESULT RESULT PRESULT 
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                                                                                                                                                                                                     Query Match 33.0%;
Best Local Similarity 54.0%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRF2 MOUSE STANDARD; PRT; 501 AA. P39479; C1-FEB-1995 (REL. 31, CREATED) C1-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) C1-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE) TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2).

MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94349371.

ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;

CELL T8:681-692(1994).

-!- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPI

OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.

-!- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.

-!- SUBLIBARTY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                 ZINC-FINGER; COILED COIL.
ZN_FING 34 72
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00518; ZINC_FINGER_C3HC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                      SEQUENCE
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leqkiatfenivcvlnrevervavtaeacsrqhrldqdkiealsnkvqqlersiglkdla 334
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                                                                                      LEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKDQV 242
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Pred. No. 3.50e-163;
61; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                    C3HC4-TYPE.
                                                                                                                 41;
                                                                                                                                                                                                                                                              Length 501;
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                                                                                                                                                                                                     Indels
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KW HYDROLASE; METALLOPROTEASE; ZINC; GLYCOPROTEIN; TRANSMEMBRANE; KW ZYMOGEN; SIGNAL; EGF-LIKE DOMAIN; 3D-STRUCTURE.	
PROSITE; PS00740; MAM.	
PDB; liAF; 31-AUG-94.	
EMBI EMBI	
-!- SIMILARITY: CONTAINS A MAM DOMAIN.	_
CC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.	
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A	_
SALIVARY DUCTS.	_
-!- TISSUE SPECIFICITY: KIDNEY, INTESTI	
DETERMINE WHICH OLIGOMER(S) WILL BE FORMED (STRAIN-SPECIFIC	
ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS,	_
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	_
-!- COFACTOR: ZINC.	_
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE SUBSTRATES	
BIOCHEMISTRY 30:8488-8493(1991).	
RA WOLZ R.L., HARRIS R.B., BOND J.S.;	
[3]	
RA DUMERMUTH E., STERCHI E.E., JIANG W., WOLZ R.L., BOND J.S.,	
MEDLINE; 92042028.	
SEQUENCE	
RN [2]	
BOND J.S.;	
MEDLINE; 92250517.	
STRAIN=C57BL/6, AND C3F	
AND PARTIAL	
EUTHERIA; RODENTIA.	_
EUK	_
GN MEPIA.	
(MEP-1).	
HA-SUE	
01-DEC-1992 (REL. 24,	
01-DEC-1992 (REL. 24, CREATED)	
P28825; .	
TD MEDA MOUSE STANDARD: PRT: 760 AA	
QY 363 SEQREQSETIVASGCELFFELSKIQSEKHAYVKDDTWFLKCIVD 406	_
Db 455 sfqrpvsdmniasgcplfcpvskmea-knsyvrddaifikaivd 497	
Qy 303 YLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPDLSSA 362	_
Db 395 ylngdgtgrgthlslffvvmkgpndallqwpfngkvtlmlldhnnrehvidafrpdvtss 454	
Qy 243 LGKLEHSLKLMEEASFDGTFLMKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCLRL 302	_

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RESULT RESULT OF THE PROPERTY 
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Best Local S
Matches 2
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P13458;
01-JAN-1990
01-JAN-1990
01-NOV-1995
EXONUCLEASE :
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                  SEQUENCE OF 378-1048 FROM N.A. MEDLINE; 92078081.
REEDER T., SCHLEIF R.;
                                                                                                                                                                                                                                                                                                   ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
PROPEP
                                                                                                                                       STRAIN=K12;
MEDLINE; 90045931.
NAOM I.S., MORTON S.J., LEACH D.R.F., LLOYD R.G.;
NUCLEIC ACIDS RES. 17:8033-8046(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
J. BACTERIOL. 173:7765-7771 (1991).
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 5.0%; l Similarity 32.9%; 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (REL. 13, CREATED)
(REL. 13, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
SBCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                760 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
CATALYTIC (ASTACIN DOMAIN).
MAM.
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 148; DB 5; Length 760;
Pred. No. 7.90e-07;
22; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
ZINC (CATALYTIC)
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2920193 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1048 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ψ
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SELECT CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CHARACTERIZATION.  MEDLINE; 93146416.  LEACH D.R.F., LLOYD R.G., COULSON A.F.;  GENETICA 87:95-100(1992).  -!- FUNCTION: AFFECTS GENETIC RECOMBINATION AND THE VIABILITY OF DNA PALINDROMES IN E.COLI. SBCC MAY HAVE A NUCLEASE ACTIVITY THAT IS FUNCTIONALLY RELATED TO ONE OF THE NUCLEASE ACTIVITIES OF THE RECBCD ENZYME.  -!- SIMILARITY: CONTAINS A COILED COIL MYOSIN-LIKE STRUCTURE. EMBL; X15981; X15981. EMBL; X15981; M64787. PIR; JS0350; BVECSC. PIR; JS0350; BVECSC. ECOGENE; EG10927; SBCC. HYDROLASE; NUCLEASE; ATP-BINDING; COILED COIL. NP BIND 37 44 ATP (POTENTIAL). SEQUENCE 1048 AA; 118721 MW; 4953805 CN;
Дu Ма	Query Match 4.3%; Score 127; DB 7; Length 1048; Best Local Similarity 34.7%; Pred. No. 7.06e-04; Matches 26; Conservative 14; Mismatches 31; Indels 4; Gaps 4;
Dy B	373 sqqtsdrehlrqwqqqlthaeqklnalaaitltltad-evat-alaqhaeqrpl-rqhlv 429   : :   :   :         :
\$ B	430 alhgqivpqqkrlaq 444 :  ::1      224 SIEQRVVEIQQTIAQ 238
RESULT ID S AC Q DT 0 DT 0 DT 0 DT 0	LT 5 SPCB DROME STANDARD; PRT; 2291 AA. Q00963; Q1-ARR-1993 (REL. 25, CREATED) Q1-ARR-1993 (REL. 25, LAST SEQUENCE UPDATE) Q1-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) SPECTRIN BETA CHAIN.
<b>2</b> 2 2 5	DROSOPHILA MELANOGASTER (FRUIT FLY). EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA. [1]
2 7 2 2 2 2 2	SEQUENCE OF 1-800 FROM N.A. MEDLINE; 90009037. BYERS T.J., HUSAIN-CHISHTI A., DUBREUIL R.R., BRANTON D., COLDSTEIN L.S.; J. CELL BIOL. 109:1633-1641(1989).
R R R R R	SEQUENCE FROM N.A.  MEDLINE; 92335263.  BYERS T.J., BRANDIN E., LUE R., WINOGRAD E., BRANTON D.;  PROC. NATL. ACAD. SCI. U.S.A. 89:6187-6191(1992).  [3]
	STRUCTURE BY NMR OF 2145-2262.  ZHANG P., TALLURI S., DENG H., BRANTON D., WAGNER G.;  STRUCTURE 0.0-0/1045)
8881	-!- FUNCTION: SPECTRIN IS THE MAJOR CONSTITUENT OF THE CYTOSKELETAL -!- FUNCTION: SPECTRIN IS THE ERYTHROCYTE PIASMA MEMBRANE. IT ASSOCIATES WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF
88	THE ERYTHROCYTE PLASMA MEMBRANE!- SUBUNIT: NATIVE SPECTRIN MOLECULE IS A TETRAMER COMPOSED OF TWO

1006:47

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                        SWAROOP A., SWAROOP M., GAREN A.;
PROC. NATL. ACAD. SCI. U.S.A. 84:6501-6505(1987).
                                                                                                                                                                                                                                                                                   DY15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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                                       -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SUBUNIT: CONSIST OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
                                                                                                                                                                                                                                           01-JAN-1990
                                                                                                                                                                                                                                                                      P13496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
-!- SIMILARITY: CONTAINS A CAP-GLY DOMAIN.
-!- SIMILARITY: STRONG, TO VERTEBRATE DYNACTIN.
                                                                                                                                                                                                     PROTEIN)
                                                                                                                                                                                                               01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
150 KD DYNEIN-ASSOCIATED POLYPEPTIDE (DP-150)
                                                                                                                                                                                                                                                         01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00019; ACTININ_1.
PROSITE; PS00020; ACTININ_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT AND THE N-TERMINUS OF THE BETA SUBUNIT.
-!- SIMILARITY: TO ALPHA ACTININ AND DYSTROPHIN.
-!- SIMILARITY: CONTAINS A PH DOMAIN.
                                                                                                                      MEDLINE; 87317680.
                                                                                                                                                             EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50003; PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLYBASE; FBGN0003471; SPEC-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M92288; M92288.
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                          DROSOPHILA MELANOGASTER (FRUIT FLY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAPPING
                                                                                                                                                                                                                                                                                                                                       251
                                                                                                                                                                                                                                                                                                                                                               850 klmsea--dgvegw-ikektk 867
                                                                                                                                                                                                                                                                                                                                                                                         192
                                                                                                                                                                                                                                                                                                                                                                                                                                             134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      737
                                                                                                                                                                                                                                                                                                                                                                                                                   795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTIPARALLEL HETERODIMERS JOINED HEAD TO HEAD SO THAT EACH END OF THE NATIVE MOLECULE INCLUDES THE C-TERMINUS OF THE ALPHA
                            INTERMEDIATE AND LOW MASS POLYPEPTIDES
                                                                                                                                                                                                                                                                                   DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A46147; A46147
                                                                                                                                                                                                                                                                                                                                       RLMEEASFDGTFLWKITNVTK 271
                                                                                                                                                                                                                                                                                                                                                                                         NIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQ-TLAQKDQVLGKLEHSL
                                                                                                                                                                                                                                                                                                                                                                                                                 evidalhkqae-s-lklnea-ekanvdk-rleaidnrykeltelaklrkqrlldalsl-y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lenaveyfqlfadaddvdnwmldtlrivssedvgrdeanvqsllk-kh-kdvadelknya 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1DRO; PRELIMINARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A33657; A33657.
                                                                                                                                                                                                                                                                                                                                                                                                                                            LERNLSELQLQAAVEATGDLEVDCYRAPCCE--SQEELALQHLVKEKLLAQLEEKLRVFA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 4.1%;
Similarity 27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETON; MEMBRANE; CALMODULIN-BINDING; ACTIN-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                             METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36
269
380
495
606
712
                                                                                                                                                                                                                                                      (REL. 13,
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                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268
379
494
605
711
                                                                                                                                                            ARTHROPODA; INSECTA; DIPTERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265785 MW;
                                                                                                                                                                                                                                                         CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.
3.
5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18087143 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 6.00e-03;
                                                                                                                                                                                                                                                                                   1319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 13;
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                                                                  Best
                                                     Matches
                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.9%;
Best Local Similarity 25.0%;
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01-MAR-1992
01-DEC-1992
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                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                    P24712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLYBASE; FBGN0001108; GL. PROSITE; PS00845; CAP_GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J02932; J02932.
PIR; A28313; A28313.
                                                                                                         SEQUENCE
                                                                                                                                                                         IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE -!- TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND
                                                                                                                                                                                                                                                                      MEDLINE; 92114750.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           EUTHERIA;
                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                    SAGUINUS OEDIPUS (COTTON-TOP TAMARIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                      KERATINOCYTE; REPEAT.
                                                                                                                                                                                                                                                         PHILLIPS M., RICE R.H.,
                                                                                                                                                                                                                                                                                    TISSUE=VAGINAL FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                   INVOLUCRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                  INVO_SAGOE
                                                                                                                                                                                                                            -!- FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 lvrlrdlsahdkhdigklskelemkrsevtelertkeklsa-kideleaivadlqeqvda 484
                                                                                                                                 PROSITE; PS00795; INVOLUCRIN.
  164
                       229 eggselpeggrggpkylegeegglkhleegkgglkhleheegglelpegvggpkhlegle 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 LQQTLAQKDQVL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 ldlangakkevl 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 QHLVKEKLLAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 a-lgaeemveqlaekkmeledkvklleeei-a-qlealeevheqlvesnheleldlre-e 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 LAVIKEWKSSPGSNIGSAPMALERNISEI-QIQAAVEATGDLEVDCYRAPCCESQEEIAI 171
                                                                  Local Similarity
                                                                                                                                                            OTHER STRATIFIED SQUAMOUS
                                                                                                                                                                                                                                          LIPS M., RICE R.H., DJIAN P., GREEN H.;
BIOL. EVOL. 8:579-591(1991).
 ESQEELALQHLVKEKLLAQLEEKLRVFANIVAVLNK-EVEASHLALAASIHQS-QLDR-E 220
                                                                                                                                                M67477; M67477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN; MICROTUBULES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                     29;
                                                                                                                                                                                                                                                                                                                            PRIMATES
                                                                                                        493 AA;
                                                                                                                                                                                                                                                                                                                                                                                           (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1319 AA;
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56
134
255
994
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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98
167
564
1124
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                                                                  29.6%;
                                                                                                        57920 MW;
                                                                                                                                                                                                                                                                                                                                       CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147858
                                                                              3.8%;
                                                   Score 112; DB 4; Le
Pred. No. 6.32e-02;
24; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 115; DB 3;
Pred. No. 2.65e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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SER-RICH.
COILED COIL.
COILED COIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SER-RICH.
                                                                                                                                                              EPITHELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                      VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                        1086880 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8197543 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                   493 AA.
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                                                                             Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1319;
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                                                     Indels
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Best Local S
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                                                                                                                                          01-MAR-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                           INVO A01
P24708;
TSENG H., GREEN H.;
MOL. BIOL. EVOL. 6:460-468(1989).
-!- FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS
IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL
                                                    SEQUENCE FROM N.A. MEDLINE; 90014142.
                                                                                        EUTHERIA; PRIMATES
                                                                                                    EUKARYOTA; METAZOA;
                                                                                                                 AOTUS TRIVIRGATUS (NIGHT MONKEY) (DOUROUCOULI)
                                                                                                                             INVOLUCRIN
                                                                                                                                                                  01-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S22695; S22695.
MIM; 179838; 11TH EDITION.
PROSITE; PS00845; CAP_GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X64838; X64838.
EMBL; M97501; M97501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- ALTERNATIVE PRODUCTS: IT IS PROBABLE THAT THE TWO FORMS OF THE PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING OF A SINGLE GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOSKELETON.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIERRE P., SCHEEL J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOSKELETON; MICROTUBULES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 11:2103-2113(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS A LARGE COILED-COIL ALPHA HELICAL DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS A CAP-GLY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          222
                                                                                                                                                                                                                                                                 509 alrvqe-vaelrrrl-esnkpagdvdmslsllqeis 542
                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                 451 tkgdletqtklehari-keleqsl-lfektkadklqreledtrvatvseksrimelekdl 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUVTURALLY SIMILAR TO THOSE FOUND IN IF AND MYOSINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF HODGKIN'S DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES
                                                                                                                                                                                                                                          LLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEAS
                                                                                                                                                                                          AOTTR
                                                                                                                                                                                                                                                                                           SQEELALQ-HLVKEKLLAQLEEKLRVFANIVAV-LNKEVEASHLA-LAASIHQSQLDREH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70:887-900 (1992)
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                                                                                                    CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                    3.8%;
                                                                                                                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                CREATED)
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                                                                                                                                                                                                                                                                                                                                         Score 113; DB 7; 1
Pred. No. 4.74e-02;
31; Mismatches 34:
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                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN SHORT FORM)
D -> E (IN REF. 2).
MW; 9446135 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAP-GLY
                                                                                                                                                                                         PRT;
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US-08-446-915-2.nsp

PROSITE; PS00795; INVOLUCRIN. EMBL; M25313; M25313 -!- TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND

MEMBRANE PROTEINS BY TRANSCLUTAMINASE. ALL THAT RESULTS IN THE FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.

OTHER STRATIFIED SQUAMOUS EPITHELIA.

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (REL. 19, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
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                                                                                                                                    PLUNKETT G. III;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: MEMBER OF THE TWO-COMPONENT RECULATORY SYSTEM ARCB/ARCA
                                                                                                                                                                                                                                             STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                        P22763;
                                                                                                                                                                                                                                                                                                                                                                                    ARCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT SITE
                                 EMBL; X53315; X53315.
                                                                            (PROBABLE).
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                                                                                         STRAIN=K12 / MG1655;
                                                                                                                                                                                                          MOL. MICROBIOL. 4:715-727(1990).
                                                                                                                                                                                                                   MEDLINE; 90355832.
                                                                                                                                                                                                                                                                               ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                         PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                    ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                            AEROBIC RESPIRATION CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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ECOGENE; EG10062; ARCB
           PIR; S11794; RGECAR.
                    EMBL; U18997; U18997.
                                                        -!- SIMILARITY: IN ITS C-TERMINUS, TO THE N-TERMINAL REGION
                                                                                                     -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 gqt-tvysppfyssk-gyaf--qinl--dltsp-tnvglyfhlisganddqlqwpcpwqq 496
|:| :::||:||:| || : : | | :: |:::|: : | | | | | | :
279 GRTVSLFSPAFYTAKYGYKLCLRLYINGDGSGKKTHLSLFIVIMRGEYDALLPWPF-RNK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                  338 VTFMLLDQN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                       497 atmtlldqn 505
                                             REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS
                                                                    KINASES
                                                                                                                MODULON. ACTIVATES ARCA BY PHOSPHORYLATION.
                                                                                                                            SENSOR-REGULATOR PROTEIN FOR ANAEROBIC REPRESSION
                                                                                                                                                                                                                                                                                                                                                                                    ECOLI
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                                                                                                                                                                                                                    FUJIWARA T., LIN E.C.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 106; DB 5;
Pred. No. 3.44e-01;
                                                                                                                                                                                                                                                                                                                            SENSOR PROTEIN ARCB
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                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                     776 AA.
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SENSORY TRANSDUCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;

INNER MEMBRANE;

TRANSCRIPTION REGULATION.

DOMAIN

CYTOPLASMIC (POTENTIAL) .

POTENTIAL.

PERIPLASMIC (POTENTIAL) CYTOPLASMIC (POTENTIAL)

POTENTIAL.

TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEMBRANE;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                               PC17 HUMAN
Q01850;
                                                  01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
PARANEOPLASTIC CEREBELLAR DEGENERATION-ASSOCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THMEL;
                             PCD17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992
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HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS
IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO
MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHILLIPS M., RICE R.H., DJIAN P., MOL. BIOL. EVOL. 8:579-591(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92114750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=ESOPHAGEAL FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEBUS ALBIFRONS (WHITE-FRONTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P24709;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KERATINOCYTE; REPEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVOLUCRIN.
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                                                                                                                                                                                                                                                                                                           219 R-E-HLLSLEQRVVELQQTLAQKDQVLGKLEH
                                                                                                                                                                                                                                                                                                                                                                                                                           267 qqegqlehleqqegelkh-leqcegqlehleq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE. TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND OTHER STRATIFIED SQUAMOUS EPITHELIA.
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Pred. No. 2.61e-01
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Search completed: Tue Dec  $10\ 07:03:42\ 1996$  Job time :  $16\ secs$ .

\*

(MT)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 10 07:03:59 1996; MasPar time 17.22 Seconds 603.847 Million cell updates/sec

Tabular output not generated.

Run on:

>US-08-446-915-2 (1-409) from US08446915.pep 2945

Description: Perfect Score:

1 MASSSAPDENEFQFGCPPAP.....KHAYVKDDTMFLKCIVDTSA 409

Scoring table: PAM 150 Gap 11

Searched: 82130 seqs, 25426960 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir47

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc

14:unrev

Statistics: Mean 47.486; Variance 124.260; scale 0.382

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		офо					
Result		Query					
No.	Score	Match	Match Length DB	8	ID	Description	Pred. No.
1	2589	87.9	416	=	B55649	TNFR-associated prot	0.00e+00
2	956	32.5	501	12	S56163	tumor necrosis facto	3.02e-125
ω	794	27.0	568	11	A55649	TNFR-associated prot	
4	148	5.0	760	12	A40195	meprin A (EC 3.4.24.	
s	144	4.9	748	12	S24134	endopeptidase 2 (EC	
6	127	4.3	1048	ω	BVECSC	sbcC protein - Esche	
7	120	4.1	2291	ა	A46147	spectrin beta chain	
8	119	4.0	714	11	539464	PABA peptide hydrola	1.13e-01
9	115	3.9	1319	10	A28313	glued protein - frui	
10	115	3.9	3259	11	S37536	macrogolgin - human	
11	115	3.9	3259	=	A56539	giantin - human	
12	111	3.8	700	Ξ	S49383	meprin A (EC 3.4.24.	7.59e-01

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8 sprpapdenefpfgcpptvcqdpkepralccagclsenprngedqicpkcrgedlqsisp

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A45592 A43360	S16129	S09331	A47212	A41642	S26365	A48246	F64058	RQECN	S03744	S03214	A36014	A47297	TNBEEH	A26572	S52487	A57281	S24545	A40448	UFEC	A49833	C24263	A24263	S28261	A43336	RGECAR	A48040	A42908	S33377	S27770	S22695	CNMVJA
liver stage antigen inositol 1,4,5-trisp	dynein-associated pr	myosin beta heavy ch		ctin - chic	P100 protein - Therm	ethylene-response pr	ä	_	•		heavy	myosin heavy chain f	97K alpha trans-indu	bsg25D protein - fru	CHO2 antigen - Chine	kinesin-like motor p	intermediate filamen	DNA-binding protein	fumarate hydratase (	autoantigen recogniz	myosin heavy chain,	myosin heavy chain,	kinesin-related prot	microtubule-vesicle	aerobic respiration	ta c	w	P63 protein - human	hypothetical protein	restin - human	pol polyprotein – sh
7.31e+00 1.13e+01	7.31e+00	9.09e+00	9.09e+00	1.13e+01	7.31e+00	7.31e+00	9.09e+00	7.31e+00	9.09e+00	9.09e+00	4.70e+00	5.86e+00	4.70e+00	•	3.76e+00	3.76e + 00			4.70e+00	4.70e+00	3.76e+00	4.70e+00	1.91e+00	3.00e+00	3.00e+00		2.40e+00	2.40e+00	9.58e-01	4.75e-01	6.01e-01

# ALI GNMENTS

1;	1; Gaps		_	Indels		25;	set	38; Mismatches 25;	, Mi		ative	serv	Con	Matches 345; Conservative	hes	Matc	
			416;	Length 416;	Len	91;	B (	Score 2589; DB 11;	ore 2		87.9%;	÷	ייי דיי	ch ch	Query Match	Quer	
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										9261	GB: U1	Sec	feren	##cross-references GB:U19261	##crc		
									NOS	1-416 ##label MOS	16 ##	1-4		##residues	##res		
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								į.	eff,	T.; Ware, C.; Kieff, E.	re, C	; Wa	.⊐				
le,	nArsda	Var		11, 1	nchi	lama	Ya	Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale,	enbac	Birk	G.;	alos	Mosi	••	#authors	#au	
												9	A55649		NCE	REFERENCE	_
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	1	1									23-Mar-1995	-Mar	23				
	hange	ც	text	95 #1	r-19	3-Ma	ກ 2	23-Mar-1995 #sequence revision 23-Mar-1995 #text change	nce r	seque	995 #	lar-1	23-M			DATE	_
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						uman	۱ 5	TNFR-associated protein EBI6 - human	oteir	ed pr	ociat	-ass	TNFR			TITLE	
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US-08-446-915-2.rpr

Gaps 1;	Query Match 32.5%; Score 956; DB 12; Length 501; Best Local Similarity 53.6%; Pred. No. 3.02e-125; Matches 120; Conservative 58; Mismatches 45; Indels 1; G	
	KEYWORDS zinc finger SUMMARY #length 501 #molecular-weight 55842 #checksum 5395	
73	nolecule residues cross-re	
	<pre>##residues 1-42,63-342,363-501 ##label SOW ##cross-references EMBL:U12597 #accession S58926</pre>	
asmic	#description Association of a RING finger protein with the cytoplasmic domain of the human type 2 TNF receptor.	
	rs Song, H.Y.; Donner, D.	
	ferences EMBL:U1259 S58925	
	<pre>##molecule type mRNA ##residues     1-501 ##label SON</pre>	
receptor.	the human type-2 tumour necrosis factor	
asmic	em. J. (1995) 309:825-829 iation of a RING finger protein with the	
	rs Song, H.Y.	
	ACCESSIONS S56163; S58925; S58926 REFERENCE S56163	
nge	#formal_name 10-Oct-1995 #	
human	Tumor necrosis factor receptor-associated protein - ALTERNATE NAMES TNF receptor-associated protein	
•	T 2 \$56163 #ty	
	Qy 361 SASFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVDTSA 409	
	Db 368 sasfqrpqsetnvasgcplffplsklqspkhayvkddtmflkcivetst 416	
S 360	Qy 301 RLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPDLS	
s 367	Db 308 rlylngdgtgkrthlslfivimrgeydallpwpfrnkvtfmlldqnnrehaidafrpdl	
T 300	Qy 241 QVLGKLEHSLRIMEEASFDGTFLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCL	
1 307	Db 248 qalgkleqsirlmeeasfdgtflwkitnvtrrchesacgrtvslfspafytakygyklc	
D 240	Qy 181 AQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKD	
d 247	Db 188 aelegklrvfenivavinkeveashlalatsihqsqldrerilsleqrvvelqqtlaqk	
L 180	Qy 121 SSPGSNIGSAPMALERNISELQIQAAVEATGDLEVDCYRAPCCESQEELALQHIVKEKLL	
1 187	Db 128 arlgcglesgpmalegnlsdlqlqaavevagdlevdcyrapcsesgeelalqhfmkekll	
K 120	Qy 62 GSPL-TQEKVHSDVAEAEIMCDFAGVGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKEMK	
k 127	Db 68 gsrirtqekahpevaeagigcpfagvgcsfkgspqsvqehevtsqtshinlllgfmkq	
P 61	Qy 2 ASSSAPDENEFQFGCPPAPCQDPSEPRVLCCTACLSENLADDEDRICPKCRADNLHPVSP 61	3

QY 97 MQEHEATSQSSHLYLLLAVLKEWKSSPGSNLGSAPM-ALERNISELQLQAAVEATGDLEV 155
Db 248 ikaheassavqhvnllkewsnslekkvsllqnesveknksiqslhnqi-csfeiei 302 :
Qy 40 LRDDEDRICPKCRADN-LHPVSPGSPLTQE-KVH-SDVAEAEIMCPFAGVGCSFKGSPQS 96
Db 189 lqkhedtdcp-cvvvscphkcsvqtllrselsahlsecvnapstcsfkrygcvfqgtnqq 247
Query Match 27.0%; Score 794; DB 11; Length 568; Best Local Similarity 38.8%; Pred. No. 9.73e-100; Matches 149; Conservative 93; Mismatches 118; Indels 24; Gaps 18;
53-91
##note nucleotide sequence not given KEYWORDS coiled coil
##molecule ##residues
title And
al J. Biol. Chem. (1994) 269:30069-30072
A55135 A5135 A5136 A5136 A5136 A5137
s-references GB:U19260
##molecule_type_mRNA ##residues
faccession A55649
<pre># journal Cell (1995) 80:389-399 #title The Epstein-Barr virus transforming protein LMP1 engages</pre>
T.; Ware, C.; Kieff, E.
A55649; A55135
DATE 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-Apr-1995
E_NAMES
A55649 #type complete
RESULT 3
Qy 363 SEQREQSETNVASGCPLFEPLSKLQSPKHAYVKDDTMFLKCIVD 406
Db 455 sfqrpvndmniasgcplfcpvskmea-knsyvrddaifikaivd 497
Qy 303 YINGDGSGKKTHLSIFIVIMRGEYDALLEWPFRNKVTFMLLDQNNREHAIDAFRPDLSSA 362
Db 395 ylngdgtgrgthlslffvvmkgpndallrwpfnqkvtlmlldqnnrehvidafrpdvtss 454
Qy 243 LGKLEHSLRIMEEASFDGTFLMKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKICIRL 302
Db 335 madleqkvlemeastydgvfiwkisdfprklqeavagripaifspafytsrygykmclri 394
Qy 183 LEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKDQV 242
rvamtaeacsrqhrldqdki

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 DCYRAPCCESQEE-LALQHLVK-E-KLLAQLEEKLRVF-AN-IVA-VLNKEVEA--SHLA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 erqkemlrnneskilhlqrvidsqaeklkeldkeirpfrqnweeadsmkssveslqnrvt 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references GB:M74897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
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                                                                                                                                                                                  #superfamily astacin homology; MAM homology
                                                                                                                                                                                                                                                                                                                                             Dumermuth, E.; Sterchi, E.E.; Jiang, W.; Wolz, R.L.; Bond,
J.S.; Flannery, A.V.; Beynon, R.J.
J. Biol. Chem. (1991) 266:21381-21385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A40195
                                                                                                                                                                                                                                                                                 B41196
#length 760
                                                                                                                                                                                                                                                                                                                          The astacin family of metalloendopeptidases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The alpha subunit of meprin A. Molecular cloning and sequencing, differential expression in inbred mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. (1992) 267:9185-9193
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16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strains, and evidence for divergent evolution of the alpha and beta subunits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             part of this sequence, including the amino end of the
                                                                                                                                                                                                                               77-275 ##label DUM
                 #domain MAM homology #label MAM
                                           #domain astacin homology #label AST\
                                                                                      #domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label PRO\
#product meprin A alpha chain #status experimental
                                                                    #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                        mature protein, was confirmed by protein sequencing
#molecular-weight 85702
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#checksum 4733
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Best Local Similarity 26.9%;
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156,160,166
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Best Local Similarity 32.9%;
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#title
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                                                                                                                                                                                                                                                            493 sgdndvilewpveneqaimtildqepdarnrmslslmfttskyq 536
                                                                                                                                                                                                                                                                                                                        323 RGEYDALLPWPFRNKVTFM-LLDQNNREHAIDAFRPDLSSASFQ 365
                                                                                                                                                                                                                                                                                                       263 LWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCLRLYLNGDGSGKKTHLSLFIVIM 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily MAM homology; astacin homology
                                                                   #formal_name Escherichia coli
30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change
                                                                                                                   BVECSC #type complete
sbcC protein - Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #binding_site zinc (His) #status predicted
#length 748 #molecular-weight 85138 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corbeil, D.; Gaudoux, F.; Wainwright, S.; Ings
A.J.; Boileau, G.; Crine, P.
FEBS Lett. (1992) 309:203-208
Molecular cloning of the alpha-subunit of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Rattus norvegicus #common_name Norway rat
02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change
Naom, I.S.; Morton, S.J.; Leach, D.R.F.; Lloyd, R.G.
                      JS0349
                                       JS0350; A43750; S27548; S06604
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Pred. No. 1.93e-04;
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Pred. No. 6.60e-05;
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Best Local Similarity 34.7%;
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cross-references MUID:92335263
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                                                                                                                                                                                                                                                                                                                                                                                               430 alhgqivpqqkrlaq 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 sqqtsdrehlrqwqqqlthaeqklnalaaitltltad-evat-alaqhaeqrpl-rqhlv 429
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This protein interacts with long DNA palindromes and reduces the viability of the carrier DNA; it is also involved in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues 379-1048 ##label RE2
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submitted to the EMBL Data Library, May 1991
S27548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily sbcC protein coiled coil; DNA repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mapping, sequence, and apparent lack of function of araJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. (1991) 173:7765-7771
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Molecular organization of sbcC, a gene that affects genetic
recombination and the viability of DNA palindromes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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#length 1048  #molecular-weight 118720  #checksum 3454
                    The complete sequence of Drosophila beta-spectrin reveals supra-motifs comprising eight 106-residue segments.
                                                                Proc. Natl. Acad. Sci. U.S.A. (1992) 89:6187-6191
                                                                                                           Byers, T.J.; Brandin, E.; Lue, R.A.; Winograd,
                                                                                                                                    A46147
                                                                                                                                                     A46147; A33657
                                                                                                                                                                                            03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                                                                                                                        spectrin beta chain - fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #type complete
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                                                                                                           E.; Branton,
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#accession #status A46147 preliminary US-08-446-915-2.rpr

Dec 10 06:47

#fresidues #molecule\_type DNA 1-2291 ##label BYE

##cross-references NCBIP:108607 ##note sequence extracted from NCBI backbone

REFERENCE #authors Byers, T.J.; Husain-Chishti, A.; Dubreuil, R.R.; Branton, D.; A33657

#journal
#title Goldstein, L.S.B. J. Cell Biol. (1989) 109:1633-1641

#accession ##status A33657 preliminary

##residues ##molecule type mRNA 1-800 ##label BY2

CLASSIFICATION #superfamily spectrin beta-G chain; alpha-actinin ##cross-references GB:M92288 actin-binding domain homology; pleckstrin repeat homology;

FEATURE 49-267 spectrin/dystrophin repeat homology #domain alpha-actinin actin-binding domain homology

SUMMARY 417-522 2146-2257 #length 2291 #domain spectrin/dystrophin repeat homology #label SN2\ #label ACT\

Matches Query Match 4.1%; Best Local Similarity 27.7%; 39; Conservative Score 120; DB 5; Pred. No. 8.87e-02; 36; Mismatches 53; Indels 13; Gaps DB 5; Length 2291; 11;

Š 밁 134 LERNISELQLQAAVEATGDLEVDCYRAPCCE--SQEELALQHLVKEKLLAQLEEKLRVFA 191 737 lenaveyfqlfadaddvdnwmldtlrivssedvgrdeanvqsllk-kh-kdvadelknya 794

В 192 NIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQ-TLAQKDQVLGKLEHSL 250 795 evidalhkqae-s-lklnea-ekanvdk-rleaidnrykeltelaklrkqrlldalsl-y 849 --------=

S В 251 RIMEEASFDGTFLWKITNVTK 271 850 klmsea--dgveqw-ikektk 867

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RESULT ENTRY TITLE ACCESSIONS ORGANISM PABA peptide hydrolase alpha chain — human #formal\_name Homo sapiens #common\_name man 19-May-1994 #sequence\_revision 17-Nov-1995 #text\_change S39464 S39464 01-Dec-1995 #type complete

REFERENCE # journal
#title #accession #authors ##molecule\_type mRNA ##residues ##status S39464 Cloning of the PABA peptide hydrolase alpha subunit (PPH-alpha) from human small intestine and its expression in COS-1 cells. FEBS Lett. (1993) 335:367-375 Dumermuth, E.; Eldering, J.A.; Gruenberg, J.; Jiang, W.; 539464 Sterchi, E.E. 1-714 ##label DUM preliminary

CLASSIFICATION

#superfamily MAM homology; astacin homology

US-08-446-915-2 rpr

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ORGANISM
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Best Local Similarity 25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title Sequence analysis of the complete cDNA and encoded polypeptide for the glued gene of Drosophila melanogaster. #cross-references MUID:87317680 #accession A28313
                                                                                                                                                                                                                                                                                                                                                                 980, 1110, 1127, 1133,
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                                                                                                                                                                                                                                                                                                                                                                                   397, 590, 771, 888,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors
                                                                            172
                                                                                                              485
                                                                                                                                                    113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 sgendailewpvenrqviitildqe 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 Idlangakkevl 552
                                                                                                                                                                                      426 lvrlrdlsahdkhdiqklskelemkrsevtelertkeklsa-kideleaivadlqeqvda 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 RGEYDALLPWPFRNK-VTFMLLDQN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 LWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCLRLYLNGDGSGKKTHLSLFIVIM 322
   232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA; mRNA
                                                                                            a-lgaeemveqlaekkmeledkvklleeei-a-qlealeevheqlvesnheleldlre-e 540
   LQQTLAQKDQVL 243
                                                                         QHLVKEKLLAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVE
                                                                                                                                                  LAVLKEWKSSPGSNLGSAPMALERNLSEL-QLQAAVEATGDLEVDCYRAPCCESQEELAL 171
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Similarity 34.1%;
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glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Swaroop, A.; Swaroop, M.; Garen, A. Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6501-6505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glued protein - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
                                                                                                                                                                                                                                                                                                        #length 1319 #molecular-weight 147858 #checksum 8175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A28313
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the authors' translation is inconsistent with the nucleotide sequence in the region 907-925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-1319 ##label SWA
                                                                                                                                                                                                                                                                                                                                             #binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                    #type complete
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                                                                                                                                                                                                                         Score 115; DB 10; Length 1319; Pred. No. 2.96e-01; 35; Mismatches 58: Indel: 6.
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Pred. No. 1.13e-01;
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밁 Ş В ENTRY Ş В Ş 밁 DATE ENTRY SUMMARY REFERENCE ORGANISM RESULT SUMMARY REFERENCE ORGANISM ACCESSIONS ACCESSIONS Query Match 3.9%; Score 115; DB 11; Length 3259; Best Local Similarity 27.7%; Pred. No. 2.96e-01; Matches Matches Query Match 3.9%; Score 115; DB 11; Best Local Similarity 27.7%; Pred. No. 2.96e-01; #accession #accession #authors submission **fauthors** description ##cross-references GB:X75304 \text{\text{V}} #length 3259 #molecular-weight 376075 #checksum 267 slvgraqvvdllqqeltaaeqrnqilsqqlqqme 300 164 ESQEELALQHLVKEKLLAQLEEKLRVFANIVAVLNKEVEA-SHLALAASIHQSQLD-REH 221 208 qtqaeqaaqqvvrekd-arfetqvrlhedellqlvtqadvetemqqklrvlqrkleehee 266 ::| | | |::| | |::| ##residues ##molecule\_type mRNA 222 LLSLEQRVVEL-QQTLAQKDQVLGKLEHSLRLME 254 267 slvgraqvvdllqqeltaaeqrnqilsqqlqqme 300 164 ESQEELALQHLVKEKLLAQLEEKLRVFANIVAVLNKEVEA-SHLALAASIHQSQLD-REH 221 ##cross-references EMBL:X75304 ##residues ##molecule\_type mRNA 222 LISIEQRVVEI-QQTLAQKDQVLGKIEHSIRIME 254 ##status ##status 1 26; 26; protein. S37536 Griffiths, G.; Renz, M. submitted to the EMBL Data Library, September 1993 Macrogolgin - a new 376 kD Golgi complex outer membrane A56539 Griffiths, G.; Renz, M. Mol. Cell. Biol. (1994) 14:2564-2576 #formal\_name Homo sapiens #common\_name man
19-Oct-1995 #sequence\_revision 19-Oct-1995
19-Oct-1995 giantin - human Conservative Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, #formal\_name Homo sapiens #common\_name man
06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change Molecular genetic analyses of a 376-kilodalton Golgi complex Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, #length 3259 #molecular-weight 376075 #checksum 4495 macrogolgin -Conservative membrane protein (giantin). 06-Jan-1995 1-3259 ##label SEE preliminary 1-3259 ##label SEE preliminary #type complete 24; Mismatches 40; 24; Mismatches DB 11; Length 3259; 40; Indels 4; Indels 4; #text\_change 4495 Gaps c.; €; 4 4;

TITLE

s49383 #type complete
meprin A (EC 3.4.24.18) -

12

ORGANISM

#formal\_name Homo sapiens #common\_name man
16-Feb-1995 #sequence\_revision 12-May-1995 #text\_change

human

SUMMARY KEYWORDS

Matches Best Local Query Match

REFERENCE ACCESSIONS

S49383 S49383

26-May-1995

Dec 10 06:47

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US-08-446-915-2 rpr

CLASSIFICATION Query Match 3.8%; Score 113; DB 11; Length 1427; Best Local Similarity 25.0%; Pred. No. 4.75e-01; cross-references MUID:92289675 165 SQEELALQ-HLVKEKLLAQLEEKLRVFANIVAV-LNKEVEASHLA-LAASIHQSQLDREH 221 168 ELALQHLVKEKLLAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHL-LSLE 226 222 LLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEAS 257 509 alrvqe-vaelrrrl-esnkpagdvdmslsllqeis 542 451 tkgdletqtklehari-keleqsl-lfektkadklqreledtrvatvseksrimelekdl 508 ##cross-references EMBi:x64838
Y #length 1427 #molecular-weight 160989 #checksum 428 ##molecule\_type mRNA 227 QRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFL 263 245 prvyntglvklqtdh-lktlndfqkllgdinwirpyl 280 ##residues 24; Conservative 3.8%; Similarity 24.7%; 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change Bilbe, G.; Delabie, J.; Brueggen, J.; Richener, H.;
Asselbergs, F.A.M.; Cerletti, N.; Sorg, C.; Odink, K.;
Tarcsay, L.; Wiesendanger, W.; DeWolf-Peeters, C.; Shipman, Restin: a novel intermediate filament-associated protein EMBO J. (1992) 11:2103-2113 #formal\_name Homo sapiens #common\_name man
04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change
18-Jun-1993 Conservative endonuclease; hydrolase; nucleotidyltransferase; polyprotein; #superfamily pol polyprotein hypothetical protein 1 - African malaria mosquito (fragment) S22695; S19853 restin - human #length 870 #molecular-weight 99312 #checksum 4310 Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, formal\_name Anopheles gambiae #common\_name African malaria mosquito highly expressed in the Reed-Sternberg cells of Hodgkin's 18-Jun-1993 reverse transcriptase 1-1427 ##label BIL #type fragment #type complete Score 112; DB 3; Length 870; Pred. No. 6.01e-01; 31; Mismatches 34; 27; Mismatches 42; Indels 4; Indels 7; Gaps Gaps -: 4;

#title

# journal

ORGANISM DATE

REFERENCE

#authors

ACCESSIONS

RESULT ENTRY

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TITLE

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Best Local Similarity 35.4%;
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#title
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#start_codon
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                                                                                                                                                                                                                                                                                                                                                               #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 11dqn 505
                                                                                                                                                                   ##molecule_type genomic RNA
##residues 1-870 ##label YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 SLFSPAFYTAKYGYKLCLRLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPF-RNKVTFM 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references EMBL:X81333
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                                                                                        ##cross-references GB:M80216
T This protein is likely to be expressed as a gag-pol polyprotein.
The precise boundary between RNA-directed DNA polymerase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
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                                                                      endonuclease has not been determined.
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                                                                                                                                                                                                                                                                                    Nucleotide sequence of the jaagsiekte retrovirus, an exogenous and endogenous type D and B retrovirus of sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                   #formal name sheep pulmonary adenomatosis virus
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain MAM homology #label MAM flength 700 #molecular-weight 79458
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J. Virol. (1992) 66:4930—4939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endonuclease (EC 3.1.-.-); RNA-directed DNA polymerase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pol polyprotein - sheep pulmonary adenomatosis virus
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                                                                                                                                                                                                                                                                and goats.
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Pred. No. 7.59e-01;
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SUMMARY

Matches

DATE

ORGANISM

REFERENCE

ACCESSIONS

ENTRY RESULT

15

Ş В Ş В

Search completed: Tue Dec 10 07:04:22 1996 Job time : 23 secs.

Ş

237 AQKDQVLGKLEHSLR 251

\*

\* (MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:07:14 1996; MasPar time 20.07 Seconds 634.805 Million cell updates/sec

Tabular output not generated.

VUS-08-446-915-4 (1-501) from US08446915.pep 3702

Description: Perfect Score: Sequence: 1 MAAASVTSPGSLELLQPGFS......NSYVRDDAIFIKAIVDLTGL 501

Scoring table: PAM 150 Gap 11

82130 seqs, 25426960 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc

Statistics: Mean 48.057; Variance 117.898; scale 0.408

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No
1		88.3	501	12	S56163	tumor necrosis facto	0.00e+00
2		26.6	416	1	B55649	TNFR-associated prot	1.74e-13
ω		21.8	568	1	A55649	TNFR-associated prot	
4		6.2	458	9	A29361	DG17 protein - slime	
<b>ζ</b> 1	162	4.4	700	11	S49383	meprin A (EC 3.4.24.	~
6		4.4	760	12	A40195	meprin A (EC 3.4.24.	
7		4.3	487	w	DDBY18	DNA repair protein R	
<b>&amp;</b>		4.3	704	12	A48040	meprin beta chain pr	
9		4.2	899	4	A42908	meprin A (EC 3.4.24.	
10		4.2	748	12	S24134	endopeptidase 2 (EC	
=		4.1	1483	ω	RGBYH1	regulatory protein H	
12		4.1	1503	:	250400	CWC1 CWC1	6 150.06

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3.24e- 9.74e- 9.74e- 8.40e- 8.40e- 6.77e- 6.77e- 2.40e- 2.40e- 2.40e- 6.45e- 6.45e- 6.45e- 6.45e- 6.45e- 6.45e- 1.33e- 1.32e- 1.

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Best Local Similarity 86.6%;
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##molecule_type mRNA
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                                                                         The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor
                                                                                                                   T.; Ware, C.; Kieff, Cell (1995) 80:389-399
                                                                                                                                       Mosialos, G.; Birkenbach, M.; Yalamanchili, T.; Ware, C.; Kieff, E.
                                                                                                                                                                              A55649
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                    preliminary
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Pred. No. 0.00e+00;
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Best Local Similarity 55.4%;
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455 SFQRPVSDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD 497
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##residues 1-13
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                                                                                                                                                 ##note
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   98;
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A novel RING finger protein interacts with the cytoplasmic
                                                                                                                                                                                                                                                                                                                  A55135
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T.; Ware, C.; Kieff, E.
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A55649
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23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
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                                                                         #region RING-finger motif
jth 568 #molecular-weight
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                                     21.8%;
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                                                                         #molecular-weight 64490
                  Score 806; DB 11;
Pred. No. 3.03e-108;
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Pred. No. 1.74e-138;
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   Mismatches
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   36;
                                   Length 568;
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Y CI	30 <b>4</b> 291	250 233	192 176	135 117	79 57	Query Match Best Local Matches	cross-ref	ACCESSIONS REFERENCE #authors #journal #title	NISM E LT			501 437	441 377	w w
ъ	kqv] ::  REVER	qnh-lerv  :   : : QDHELQRL	ethykt      EVHYE\	evdqic ; ; ; TLKEYF	clmver     CLTSII	tch al Sim 64;	cross-references accession A29; ##molecule_type ##residues ORDS DNA ARY #lei	i⊷ 6i	4.	VDLTGL	vdtsdi 565	qgssrrhl : ::   : H-NNREHV	ysqpf) :  :   FSPAF)	lesqla   ; ; LSNKVÇ
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83	kqvlpkaldicsngyr ::  :: :      REVERVAVTAEACSRQHR	mymgili : ::: : ::-LALLL	idesqç :   :  LTC-DC	ncqykf   : : LCPFLL	ecc-ciy :   :  NCAACVY	rv.	nces MUID:8814 A29361 A29361 -type DNA 1-458 ## DNA binding; #length 458	A29361 A29361 Driscoll, D.M. Mol. Cell. Bic Two divergentl are cyclic A	A29361 #ty DG17 protein - #formal name D 31-Mar-1989 #s 31-Dec-1993			gdafkpdpr    :   IDAFRPDVT	ykmcar        YKMCLF	lsvhdi :::  : IGLKDI
#type	/r 319   !R 308	iek-l :   :LSSFL	csvk-  :    CCKKK	vtcsf.  : TECPA	y-s-fne   : ::  YEGLYEE	6.2%; 14.8%; htive	MUID:88142840 MUID:88142840 BONA 1-458 ##label binding; zinc:	D.M.; Biol Biol Jently Jently	#type sin - s sine Dict 39 #seqn			sssfk	WYLNG	rladm :  : .AMADL
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4.4%; Score 162; DB 11; Length 700;
Best Local Similarity 33.3%; Pred. No. 4.44e-07;
Matches 35; Conservative 33; Mismatches 22; Indels 15;
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                                         Dumermuth, E.; Sterchi, E.E.; Jiang, W.; Wolz, R.L.; Bond,
J.S.; Flannery, A.V.; Beynon, R.J.
J. Biol. Chem. (1991) 266:21381-21385
                                                                                                                                                                                                                                                                                                      G.A.; Bond, J.S.
J. Biol. Chem. (1992) 267:9185-9193
The alpha subunit of meprin A. Molecular cloning and sequencing, differential expression in inbred mouse strains, and evidence for divergent evolution of the alpha and beta subunits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 sgdndailewpvenrqaimtildge 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 77-275 ##label DUM
##cross-references GB:M74897; GB:M74238
                            ##molecule_type DNA
                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
##residues 1-4
##residues
                                                                                                                                                                                                                                                              ##cross-references EMBL:S93798
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                                                                                                                                                                             Antoine, G.; Benit, P.; Chanet, R.; Fabre, R.; Faye, G.;
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DNA repair protein RAD18 - yeast (Saccharomyces cerevisiae)
protein YCR066w
protein YCR066w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Benit, P.; Chanet, R.; Fabre, F.; Faye, G.; Fukuhara, H.;
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                                                                                                                                                                                                                               S19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of the sup61-RAD18 region on chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formal_name Saccharomyces cerevisiae
31-Mar-1991 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S05802; S22263; S19481; JS0082
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                                                                                                                                                 Fukuhara, H.; Mathieu, A.; Sor, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                         1-487 ##label BEN
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#domain propeptide #status predicted #label PRO\
#product meprin A alpha chain #status experimental
#label MAT\
   1-487 ##label ANT
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#domain MAM homology #label MAM
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Pred. No. 4.44e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Mismatches 28;
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Db 432 iwhiqnftq-ilggqdtsvysppfyssk-gy-a-fqiymdir-ystnvgiyfhli 481      :    ::  :::  ::    :::  :  :  :  Qy 355 IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYINGDGTGRGTHLSLFFVVM 414  Db 482 sganddqlqwpcpwqqatmtlldqnpdirqrmfnq-rsittdpt 524	%; Score 158; DB 12; Le 7%; Pred. No. 1.44e-06; ve 34; Mismatches 22;	reacture 72-258 #domain astacin homology #label AST\ 72-258 #domain MAM homology #label MAM 261-430 #domain MAM homology #label MAM SUMMARY #length 704 #molecular-weight 79585 #checksum 7013	#status #molecule_ #residues #cross-ref #CATION	<pre>#journal J. Biol. Chem. (1993) 268:21035-21043 #title Cloning, expression, and chromosomal localization of the</pre>	ACCESSIONS A48040 REFERENCE A48040  #authors Gorbea, C.M.; Marchand, P.; Jiang, W.; Copeland, N.G.;  Gilbert D.J.: Tenking N.B.: Rond J.S.	RESULT 8  ENTRY A48040 #type complete TITLE meprin beta chain precursor - mouse ORGANISM #formal name Mus musculus #common name house mouse DATE 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 07-Jul-1995	<pre>Db 21 qldtllrchickdflkvpvltpcghtfcslcirthlnnqp-ncplclfe 68 : ::</pre>	Query Match 4.3%; Score 158; DB 3; Length 487; Best Local Similarity 36.7%; Pred. No. 1.44e-06; Matches 18; Conservative 16; Mismatches 14; Indels 1; Gaps 1;	28-48  \$ region zinc finger motif\ 51-65  \$ region zinc finger motif\ 190-210  \$ region zinc finger motif\ 190-210  \$ region zinc finger motif\ 200-210  \$ fregion zinc finger motif\ 100-210  \$ fregion zinc finger motif\ 200-210  \$ fregion zinc finger motif\ 200-2100  \$ fregion zinc finger mot	#gene LISTA:RAD18 #fene Francisco #map position 3R CLASSIFICATION #superfamily DNA repair protein RAD18 KEYWORDS ATP; DNA binding; DNA repair; zinc finger	#accession JS0082 ##molecule_type DNA ##residues 1-487 ##label CHA	rs al -referen	REFERENCE JSOOR)
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8 Ş ENTRY Ş 뭉 SUMMARY ORGANISM ALTERNATE\_NAMES FEATURE KEYWORDS CLASSIFICATION REFERENCE RESULT ACCESSIONS ORGANISM ALTERNATE\_NAMES Query Match 4.2%; Best Local Similarity 40.0%; Matches 72-258 261-430 #title faccession # journal #authors cross-references MUID: 92317075 432 iwhiqmft---q-llgqqt-tvysppfyssk-gy-a-fqinl--ditsp-tnvglyfhli 480 415 KGPNDALLQWPFN-QKVTLMLLDHN 438 481 sganddqlqwpcpwqqatmtlldqn 505 ##molecule\_type mRNA ##status ##cross-references NCBIP:107784 ##residues 10 IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVM 414 34; endopeptidase-2 beta chain; meprin beta chain; meprin-a beta #domain MAM homology #label MAM
#length 668 #molecular-weight 75049 #checksum \*superfamily meprin A; astacin homology; MAM homology A42908 heterodimer; hydrolase Johnson, G.D.; Hersh, L.B. J. Biol. Chem. (1992) 267:13505-13512 A42908 #type complete meprin A (EC 3.4.24.18) beta chain - rat Conservative Cloning a rat meprin cDNA reveals the enzyme is a A42908 A42908 #formal\_name Rattus norvegicus #common\_name Norway rat 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change heterodimer 23-Mar-1995 sequence extracted from NCBI backbone 1-668 ##label JOH preliminary #domain astacin homology #label AST\ 23; Score 157; DB 4; Length 668; Pred. No. 1.93e-06; Mismatches 16; Indels 12; Gaps 9

ACCESSIONS REFERENCE #authors # journal \*cross-references MUID:92371675 Corbeil, D.; Gaudoux, F.; Wainwright, S.; Ingram, A.J.; Boileau, G.; Crine, P.
FEBS Lett. (1992) 309:203—208 S24134 S24134 Molecular cloning of the alpha-subunit of rat endopeptidase-24.18 (endopeptidase-2) and co-localization #formal\_name Rattus norvegicus #common\_name Norway rat 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change hybridization. with endopeptidase-24.11 in rat kidney by in situ 19-0ct-1995 J.; Kenny,

faccession

524134

##status

preliminary

Dec 10 06:51 US-08-446-915-4.rps

Ş Вþ Ω<sub>V</sub> 밁 SUMMARY FEATURE KEYWORDS CLASSIFICATION Matches Query Match 4.2%; Best Local Similarity 31.8%; 265-434 156, 160, 166 76-262 436 vwtirnisqvlentvkg-drlv-sprfynse-gygfgvtlypngritsnsgylglafhly 492 415 KGPNDALLQWPFNQKVTLM-LLDHN 438 493 sgdndvilewpveneqaimtildqe 517 ##residues 355 IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVM 414 ##molecule\_type mRNA 27; \$superfamily MAM homology; astacin homology
hydrolase; metalloprotein; proteinase; zinc #length 748 #molecular-weight 85138 #checksum Conservative #binding\_site zinc (His) #status predicted #domain MAM homology #label MAM\ #domain astacin homology #label AST\ 1-748 ##label COR Score 155; DB 12; Length 748; Pred. No. 3.45e-06; 23; Mismatches 31; Indels 31; Indels 4; 2333 Gaps 4

REFERENCE REFERENCE ORGANISM ALTERNATE\_NAMES ENTRY RESULT ACCESSIONS #accession cross-references MUID:89125585 \*accession #title Functional dissection and sequence of yeast HAP1 activator. #cross-references MUID:89106221 # journal #authors **fauthors** journal ##cross-references EMBL:J03152 ##residues ##molecule\_type DNA 11 S15447 regulatory protein HAP1 - yeast (Saccharomyces cerevisiae) regulatory protein CYP1 CYPl (HAPl) regulator of oxygen-dependent gene expression yeast. I. Overall organization of the protein sequence Creusot, F.; Verdiere, J.; Gaisne, M.; Slonimski, P.P. J. Mol. Biol. (1988) 204:263-276 A31312 S15447 Pfeifer, K.; Kim, K.S.; Kogan, S.; Guarente, Cell (1989) 56:291-301 30-Sep-1991 \*sequence\_revision 30-Sep-1991 \*text\_change A31312 A31312; S15447; S05804; S15446 formal\_name Saccharomyces cerevisiae displays several novel structural domains. 13-Sep-1995 1-1483 ##label PFE #type complete Ħ

FEATURE KEYWORDS CLASSIFICATION GENETICS 1-148 59-98 #gene ##molecule\_type DNA ##residues ##note ##cross-references EMBL:X13793 DNA binding; heme binding; zinc finger #superfamily regulatory protein HAP1; GAL4 zinc binuclear LISTA: CYP1; HAP1 cluster homology 1-62, 'R', 64-144, 'T', 146-322, 'K', 324-454, 'S', 456-507, 'V', 509-586, 'N', 588-882, 'D', 884-959, 'H', 961-1150, 'D', 1152-1156, 'S', 1158-1304, 'N', 1305-1483 #flabel CRE1 #domain DNA-binding #status predicted #label DNA\
#domain GAL4 zinc binuclear cluster homology #label the sequence is from mutant CYP1-18

#region zinc finger CCCC motif\

US-08-446-915-4 pr

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Best Local Similarity 31.6%;
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Best Local Similarity 31.6%;
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1388-1483
                                     #authors
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389-394, 415-420
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                                                                                                                                                                                                                            242 EHLALLISSFLEAQASPGT 260
                                                                                                                                                                                                                                                                                              184 KFPLTCDGCGKKKIPRETFQDHVRACSKCRV--LCRFHTVGCSEMVETENLQDHELQRLR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references EMBL:U20865
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                                                                                                                               A47380 #type complete RING finger-containing DNA binding protein RING1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, February 1995 The sequence of S. cerevisiae cosmid 9672.
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#length 1483
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                                                                                                  #formal_name Homo sapiens #common_name man
21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S59386
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                                Lovering, R.; Hanson, I.M.; Borden, K.L.; Martin, S.;
                                                                                                                                                                                                                                                                                                                                                                Conservative
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O'Reilly, N.J.; Evan, G.I.; Rahman, D.; Pappin, Trowsdale, J.; Freemont, P.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerevisiae)
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Pred. No. 6.15e-06;
23; Mismatches 29;
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<u>=</u>
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Pred. No. 6.15e-06;
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                   D.J.;
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ENTRY

ORGANISM

A44272 #type complete
photomorphogenesis repressor COP1 - Arabidopsis thaliana
formal\_name Arabidopsis thaliana #common\_name mouse-ear

30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                           Query Match 3.8%;
Best Local Similarity 32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.8%; Score 141; DB 11; Best Local Similarity 32.6%; Pred. No. 1.86e-04;
                                                                                                                                                                                                                                                                                                        43-229
232-401
                                                                                                                                                                                                                                                                                                                                                                                                                                             #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     # journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cross-references MUID: 93211912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        f journal
                                                                                                                                                     403 vwtvrnfsqv-len-tskgdklqsprfynse-gygfgvtlypnsress-g-ylrlafhvc 457
                                                                                          458 sgendailewpvenrqviitildqe 482
                                                                                                                                                                                                                                                                                                                                                                                                                        ##status
                                                       415 KGPNDALLQWPF-NQKVTLMLLDHN
                                                                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
                                                                                                                                355 IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVM 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references NCBIN:128010; NCBIP:128011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 lhselmcpicldmlkntmttkeclhrfcsdcivtalrsgnkecptc 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 LEAKYLCSACKNILRRPFQA-QCGHRYCSFCLTSILSSGPQNCAAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
 5
                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                             #superfamily MAM homology; astacin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                            S39464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. (1993) 335:367-375
Cloning of the PABA peptide hydrolase alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence extracted from NCBI backbone
#length 377 #molecular-weight 39145 #chec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A47380
                                                                                                                                                                                                                                                                                    #length 714 #molecular-weight 80703 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PABA peptide hydrolase alpha chain - human #formal name Homo sapiens #common name man 1944 #sequence_revision 17-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S39464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. (1993) 90:2112-2116
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumermuth, E.; Eldering, J.A.; Gruenberg, J.; Jiang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S39464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification and preliminary characterization of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sterchi, E.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 motif related to the zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             in COS-1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PPH-alpha) from human small intestine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-377 ##label
                                                                                                                                                                                                                                                                                                                                                                                   1-714 ##label DUM
                                                                                                                                                                                                                                                                                                      #domain MAM homology #label MAM
                                                                                                                                                                                                                                                                                                                        #domain astacin homology #label AST\
                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . . . . . . . . . . . .
                                                                                                                                                                                                       Score 139; DB 11;
Pred. No. 3.24e-04;
21; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches 16; Indels
                                                         438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOT
                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                           Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #checksum
                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                         6;
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                                                                                                                                                                                                                                                                                    3852
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Search completed: Tue Dec 10 07:08:25 1996 Job time : 71 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intellicenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 10 07:06:29 1996; MasPar time 13.19 Seconds 660.452 Million cell updates/sec

Tabular output not generated.

Run on:

Description: Perfect Score: >US-08-446-915-4 (1-501) from US08446915.pep 3702

Sequence: 1 MAAASVTSPGSLELLQPGFS......NSYVRDDAIFIKAIVDLTGL 501

Scoring table: PAM 150 Gap 11

Searched: 49340 segs, 17385503 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Statistics: Mean 50.182; Variance 93.568; scale 0.536

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

											í		Result No.
13	12	1	10	9	00	7	σ	Ç	4	w	4	_	
120	119	120	126	135	141	153	157	158	162	229	412	3702	Score
3.2	3.2	3.2	3.4	3.6	3.8	4.1	4.2	4.3	4.4	6.2	26.3	100.0	Query Match
1863	227						668						Query Match Length DB
_	<b></b>	9	9	2	7	2	S	6	თ	2	8	œ	DB
BRC1_HUMAN	TPMS HUMAN	YNN1_CAEEL	ZG48 XENLA	COP1 ARATH	RIN1 HUMAN	CYP1 YEAST	MEPB RAT	RA18 YEAST	MEPA MOUSE	DG17_DICDI	TRF1_MOUSE	TRF2 MOUSE	ID
BREAST CANCER TYPE 1	TROPOMYOSIN ALPHA CHA	HYPOTHETICAL 18.7 KD	GASTRULA ZINC FINGER	COP1 REGULATORY PROTE	RING1 PROTEIN.	CYP1 ACTIVATORY PROTE	MEPRIN A BETA-SUBUNIT	DNA REPAIR PROTEIN RA	MEPRIN A ALPHA-SUBUNI	DG17 PROTEIN.	THE RECEPTOR ASSOCIAT	TNF RECEPTOR ASSOCIAT	Description
2.21e-03	3.06e-03	2.21e-03	3.04e-04	1.40e-05	1.69e-06	2.17e-08	4.90e-09	3.37e-09	7.47e-10	1.30e-21	1.75e-178	0.00e+00	Pred. No.

1514 1514 1514 1514 1516 1516 1516 1516	Dec 10 06:50
012070000000000000000000000000000000000	0
113 1114 1110 1111 1111 1111 1111 1110 1100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 10	8
3.1 3.1 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	
400 501 501 1040 11040 11042 1458 458 479 284 284 284 284 284 284 284 284 284 284	
512884988542188815577777986	
OND THEMA  UND THEMA	US-08-4
OUTER MEMBRANE PROTEII UVS-2 PROTEIN. GASTRULA ZINC FINGER V(D) J RECOMBINATION A PARAMYOSIN (FRAMENT) ZINC FINGER PROTEIN M TYPE III INTERMEDIATE PARAMYOSIN LONG FORM TROPOMYOSIN BETA CHAI TROPOMYOSIN BETA CHAI TROPOMYOSIN, SMOOTH M MYOSIN HEAVY CHAIN, C 3-PHOSPHOSHIKIMATE 1- VIMENTIN 1 AND 2. VIMENTIN 4. ZINC-BINDING PROTEIN CHA4 ACTIVATORY PROTE MITOCHONDRIAL HEAT SH MYOSIN HEAVY CHAIN, I TROPOMYOSIN BETA CHAI TROPOMYOSIN ALPHA CHA GASTRULA ZINC FINGER KERATIN, TYPE I CYTOS TUMOR NECROSIS FACTOR VIMENTIN. TRANSCRIPTION FACTOR MYOSIN HEAVY CHAIN, G	US-08-446-915-4.rsp
2.07e-02 1.51e-02 5.24e-02 5.24e-02 5.85e-02 5.82e-02 5.176e-01 7.12e-02 1.76e-01 3.19e-01 3.19e-01 3.19e-01 3.19e-01 3.19e-01 5.73e-01 5.73e-01 5.73e-01 5.73e-01 7.64e-01 7.64e-01 7.64e-01 7.64e-01 7.64e-01 7.64e-01	

## ALI CNMENTS

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>	SQ	FT	₹	DR	DR	င္ပ	င္ပ	cc	cc	8	RL	RA	RX	RΡ	RN	8	8	SO	DE	DT	DT	DΤ	АC	Ħ	RES
	SEQUENCE 501 AA; 56026 MW; 1264825 CN;	ZN_FING 34 72 C3HC4-TYPE.	7 ZINC-FINGER; COILED COIL.	PROSITE; PS00518; ZINC FINGER C3HC4.	EMBL; L35303; L35303.	: -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	: -!- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.	: -!- SUBCELLULAR LOCATION: CYTOPLASMIC.	OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).		CELL 78:681-692(1994).	ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;	MEDLINE; 94349371.	SEQUENCE FROM N.A.	Ξ	EUTHERIA; RODENTIA.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	MUS MUSCULUS (MOUSE).	TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2).	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)	01-FEB-1995 (REL. 31, CREATED)		TRF2 MOUSE STANDARD; PRT; 501 AA.	RESULT 1

Matches

501;

Ş MAAASVTSPGSLELLQPGFSKTLLGTRLEAKYLCSACKNILRRPFQAQCGHRYCSFCLTS 60 69

120

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밁

В Ş 121 2 yescheglcpfl1tecpackglvr1sekehhteqecpkrs1scqhcrapcshvd1evhye 180 120

Ş 망 181 181 VCPKFPLTCDGCGKKKIPRETFQDHVRACSKCRVLCRFHTVGCSEMVETENLQDHELQRL 240 240

YESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHCRAPCSHVDLEVHYE

180

Ś

121

Ş 망 301 301 eacsrqhrldqdkiealsnkvqqlersiglkdlamadleqkvselevstydgvfiwkisd EACSRQHRLDQDKIEALSNKVQQLERSIGLKDLAMADLEQKVSELEVSTYDGVFIWKISD 360 360

Ş 361 FTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVMKGPNDA ftrkrqeavagrtpaifspafytsrygykmclrvylngdgtgrgthlslffvvmkgpnda 420

맑

361

밁 421 llqwpfnqkvtlmlldhnnrehvidafrpdvtsssfqrpvsdmniasgcplfcpvskmea 480

Ş 421 LLQWPFNQKVTLMLLDHNNREHVIDAFRPDVTSSSFQRPVSDMNIASGCPLFCPVSKMEA

밁 Š 481 481 knsyvrddaifikaivdltgl KNSYVRDDAIFIKAIVDLTGL 501 501

TRF 1 2 MOUSE

P39428; STANDARD; PRT;

409

8

01-FEB-1995 (REL. 31, CRE 01-FEB-1995 (REL. 31, LAS 01-FEB-1995 (REL. 31, LAS TNF RECEPTOR ASSOCIATED F (REL. 31, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE)

MUS MUSCULUS (MOUSE). FACTOR 1 (TRAF1).

EUTHERIA; RODENTIA. EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

390-402

RESULT
ACCOMMENSOR
DT 010
DT 0 SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND MEDLINE; 94349371. HENZEL W.J., GOEDDEL D.V.;

ROTHE CELL T E M., WONG S.C., 78:681-692(1994)

÷ FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR SUBCELLULAR LOCATION: CYTOPLASMIC. THE CYTOPLASMIC (TNF-R2)

DOMAIN

TRAF1 AND

-!- SUBUNIT: HETERODIMER OF L35302; L35302.

TRAF2.

EMBL; COILED COIL.

SEQUENCE 409 A 45464 š 857796 CN;

Query Match Local Similarity 26.3%; 54.0%; Pred. Score 972; No. 1.75e-178; В 8 Length 409;

> Dec 10 06:50 US-08-446-915-4.rsp

Α

Matches 183 121; Conservative 61; Mismatches 41; Indels Gaps

밁

Ş 275 leeklrvfanivavlnkeveashlalaasihqsqldrehllslegrvvelqgtlaqkdqv 242 LEQKIATFENIVCVLNREVERVAVTAEACSRQHRLDQDKIEALSNKVQQLERSIGLKDLA 334

335 243 MADLEQKVSELEVSTYDGVF IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRV lgklehslrlmeeasfdgtflwkitnvtkrchesvcgrtvslfspafytakygyklclrl 302 394

Ş 뭉

Q 문 395 303 ylngdgsgkkthlslfivimrgeydallpwpfrnkvtfmlldqmnrehaidafrpdlssa {|||||;| ||||||||||:|:| YLNGDGTGRGTHLSLFFVVMKGPNDALLQWPFNQKVTLMLLDHNNREHVIDAFRPDVTSS 454

맑 363 sfqrpqsetnvasgcplffplsklqspkhayvkddtmflkcivd 406

455 SFQRPVSDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD

Ş

STANDARD; PRT; 458 A.

DG17 DICDI P11467; 01-OCT-1989 01-OCT-1989 01-FEB-1994 (REL. 12, CREATED)
12, LAST SEQUENCE UPDATE)
28, LAST ANNOTATION UPDAT UPDATE)

ZFAA OR DG17. DG17 PROTEIN.

420

DICTYOSTELIUM DISCOIDEUM (SLIME

EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA; MOLD)

EUMYCETOZOA; DICTYOSTELIA.

SEQUENCE FROM N.A.

MEDLINE; 88142840.

DRISCOLL D.M., WILLIAMS J.G.;

MOL. GELL. BIOL. 7:4482-4489(1987).

-!- THE EXPRESSION OF DGI7 PROTEIN IS DEVI-!- INDUCTION: BY CAMP DURING AGGREGATION.

DEVELOPMENTALLY REGULATED

EMBL; M18106; M18106.

DICTYDB; PIR; A29361; A29361. DD02010; ZFAA.

TO DROSOPHILA SINA POTENTIAL. æ 71-108).

DEVELOPMENTAL PROTEIN; ZINC-FINGER.
SIMILAR 25 67 TO DROSO
ZN FING 27 66 POTENTIA
ZN FING 178 198 POTENTIA
SEQUENCE 458 AA; 53015 MM; 110734

POTENTIAL MW; 1107348 2

Query Match Best Local Matches Match Similarity 64; 6.2%; llarity 24.8%; Conservative Score 229; DB 2; I Pred. No. 1.30e-21; 68; Mismatches 103: 103; Length Indels 458 23; Gaps

79 clmverafdkkecc-ciy-s-fneqiveggtncsppdgasvqmqrnlikd-eengckeki 134

57 CLTSILSSGPQNCAACVYEGLYEEGISILESSSAFPDNAARREVESLPAVCPNDGCTWKG 116

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135 

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Ş 176 232

250 

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1006:50

US-08-446-915-4.rsp

233 QDHELQRL-REH-LALLLSSFLEAQASPGTLNQVGPELLQRCQILEQKIATFENIVCVLN

S B S

291

REVERVAVTAEACSROHR 308

304 kqv--lpkaldicsngyr 319

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01-DEC-1992
01-DEC-1992
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6, AND C3H/HE; TISSUE-KIDNEY; MEDLINE; 92250517.
                           SIGNAL
PROPEP
                                                                                                                                     EMBL; M74897; M74897.
EMBL; M82962; M82962.
                                                                                                                                                                                                                               -!- SUBUNIT: HOMOTETRAMER OF ALPHA OR BETA SUBUNITS; HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS ARE FORMED BY NON-COVALENT ASSOCIATION OF TWO DISURIDE-LINED HETERODIMERS; GENETIC FACTORS DETERMINE WHICH OLICOMER(S) WILL BE FORMED (STRAIN-SPECIFIC).
-!- PIM: N-GLYCOSYLATED; AT LEAST 3 OF THE POTENTIAL SITES ARE USED.
-!- TISSUE SPECIFICITY: KIDNEY, INTESTINAL BRUSH BORDERS, AND
  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                            WOLZ R.L., HARRIS R.B., BOND J.S.;
BIOCHEMISTRY 30:8488-8493(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                              DUMERMUTH E., STERCHI E.E., JIANG W., FLANNERY A.V., BEYNON R.J.;
J. BIOL. CHEM. 266:21381-21385(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEPA MOI
P28825;
                                                                                                                          PIR;
                                                                                                                                                              METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
-!- SIMILARITY: THE PROTEIN INCLUDES 1 EGF-LIKE REPEAT.
-!- SIMILARITY: CONTAINS A MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                               PROSITE;
                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 91355206.
                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 77-275 FROM N.A. MEDLINE; 92042028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOND J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEPRIN A ALPHA-SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEPTIDASE-2)
                                                        ZYMOGEN;
                                                                       IYDROLASE;
                                                                                   PROSITE; PS00142; ZINC_PROTEASE.
PROSITE; PS00740; MAM.
                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JIANG W., GORBEA C.M., FLANNERY A.V., BEYNON R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOL. CHEM. 267:9185-9193(1992)
                                                                                                                                                                                                                       SALIVARY DUCTS.
                                                                                                                                                                                                                                                                                                                                               PREFERENTIALLY ON CARBOXYL SIDE OF HYDROPHOBIC RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                            A40195; A40195.
liAF; 31-AUG-94
                                                       SIGNAL;
                                                      METALLOPROTEASE; ZINC; IGNAL; EGF-LIKE DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                         HARRIS R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REL. 24,
(REL. 24,
(REL. 32,
  1
34
78
78
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 33
77
760
726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
MEPRIN A ALPHA-SUBUNIT.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                       GLYCOPROTEIN;
3D-STRUCTURE.
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MEDLINE; 92221691.
BENIT P., CHANET R., F
YEAST 8:147-153(1992).
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JONES J.S., WEBER S., PRAKASH L.;
NUCLEIC ACIDS RES. 16:7119-7131(1988).
-!- FUNCTION: FUNCTIONS WITH DNA REPAIR PROTEIN RAD5 IN ERROR-FREE
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01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
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ACT_SITE
                                                                                    SEQUENCE FROM N.A. MEDLINE; 88303333.
                                                                                                                                                                       GENE 74:543-547(1988).
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                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 89232745.
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Pred. No. 7.47e-10;
25; Mismatches 28;
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Query Match

Best Local Similarity 40.0%;

Matches 34; Conservative
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Pred. No. 4.90e-09;
23; Mismatches 16;
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ZINC (CATALYTIC)
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CYP1 YEAST
P12351;
01-OCT-1989
                                                                                                                                  SACCHAROMYCES CEREVISIAE
                                                                                                                                             CYP1 ACTIVATORY PROTEIN.
                                                                                                                                                   01-NOV-1995
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                                                                                                               SEQUENCE FROM N.A.
                                                                                                                          EUKARYOTA; FUNGI;
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12, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
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                                                                                                                                 (BAKER'S YEAST).
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CREUSOT F., VERDIERE J., GAISNE J. MOL. BIOL. 204:263-276(1988).
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MEDLINE; 89125585.

GAISNE M., SLONIMSKI P.P.;

MEDLINE; 89106221. SEQUENCE FROM N.A.

PFEIFER K., KIM K.-S., KOGAN s; GUARENTE

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CELL 56:291-301(1989)

MUTANT CYP1-18.

MEDLINE; 89125586.

VERDIERE J., GAISNE M., GUIARD B., DEFRANOUX N., SIONIMSKI P.P.; J. MOL. BIOL. 204:277-282(1988).
-!- FUNCTION: REGULATION OF OXYGEN DEPENDENT GENE EXPRESSION. IT MODULATES THE EXPRESSION OF ISO-1 AND ISO-2 CYTOCHROME C.

-!- SUBCELLUIAR LOCATION: NUCLEAR.
-!- CYP1-18 MUTANT ACTIVATE THE EXPRESSION OF CYP3 (ISO-2) WHILE REDUCING THAT OF CYC1 (ISO-1)

HEME IS AN EFFECTOR MOLECULE FOR CYP1/HAP1. THE REPEAT REGION

(SEE FT TABLE) MEDIATES HEME INDUCTION BY MASKING THE DNA-BINDING

1006:50

US-08-446-915-4.rsp

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                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                          Best Local Similarity 31.6%;
                                                                01-JUN-1994 (REL. 101-JUN-1994 (REL. 101-OCT-1994 (REL. 101-OCT-1994)
                                                                                         Q06587;
                                                                                                RIN1_
                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                         RING1 PROTEIN.
                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13793; X13793.
EMBL; J03152; J03152.
PIR; S05804; RGBYH1.
                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
MEDLINE; 93211912.
                         EUTHERIA; PRIMATES
                                EUKARYOTA; METAZOA;
                                         HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T00346; -. LISTA; SC00253; CYP1.
       SEQUENCE FROM N.A.
                                                                                                                                   242
                                                                                                                                                 119 ervkslektlskvhsspss 137
                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC; METAL-BINDING; REPEAT; HEME.
                                                                                                                                                                                                                                                                                                                                                                                                                                      franscription regulation; Activator; dna-binding; nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00463; ZN2_CY6_FUNGAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD; L0002665; HAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLUSTER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN IN THE ABSENCE OF INDUCER.
                                                                                                                                 EHLALLLSSFLEAQASPGT 260
                                                                                                                                                                KFPLTCDGCGKKKIPRETFQDHVRACSKCRV--LCRFHTVGCSEMVETENIQDHELQRLR 241
                                                                                                                                                                               riplscticrkrkvkcdklrphcqqctktgvahlchymeqtwaeeaekellkdnelkklr 118
                                                                                                 HUMAN
                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                            1151
1157
1305
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299
323
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415
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323
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63
177
280
                                                                                                STANDARD;
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30,
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322
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587
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587
588
3960
                               CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                      93
189
                                                                                                                                                                         ::
                                                                                                                                                                                                                                   164150
                                                               CREATED)

LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)
                                                                                                                                                                          <u>..</u>
                                                                                                                                                                                                  23;
                                                                                                                                                                                                         Score 153; DB 2; Length 1483; Pred. No. 2.17e-08;
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                                                                                                                                                                                                                                                   S D E D Z < S X H
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7 X TANDEM REPEATS OF A REGION THAT
                                                                                                                                                                                                                                                                                                                                                                                                             ZN(2)-CYS(6), FUNGAL-TYPE.
S -> R (IN CYP1-18 MUTANT).
                                                                                                                                                                                                                                                                                                                                                                                    CONTAINS A [KR]-C-X-[ILV]-D-H MOTIF
                                                                                                PRT;
                                                                                                                                                                                                  Mismatches
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                                                                                                377 AA.
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Best Local Similarity 31.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.8%;
Best Local Similarity 32.6%;
                                                             ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COP1 ARATH P43254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.
ZN FING 19 58 C3HC4-TYPE.
DOMAIN 176 231 GLY-RICH.
DOMAIN 285 348 GLY-RICH.
DOMAIN 172 175 NUCLEAR LOCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER EMBL; Z14000; Z14000.
PIR; A47380; A47380.
                                                                           ZINC-FINGER; NUCLEAR PROTEIN; REPEAT.
ZN_FING 52 89 C3HC4-TYPE.
                                                                                                           PROSITE;
                                                                                                                       PROSITE;
                                                                                                                                      EMBL; L24437; L24437.
                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
-!- SIMILARITY: BELONGS TO THE BETA TRANSDUCIN FAMILY; CONTAINS
                                                                                                                                                                                                                                               -!- FUNCTION: ACTS AS A REPRESSOR OF PHOTOMORPHOGENESIS IN DARKNESS,
AND LIGHT STIMULI ABROGATE THIS SUPPRESSIVE ACTION. COULD FUNCTION
                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)
                                                                                                                                                                                                                                                                                                                                                                                                                                    COP1 OR FUS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOVERING R., HANSON I.M., BORDEN K.L.B., MARTIN S., EVAN G.I., RAHMAN D., PAPPIN D.J.C., TROWSDALE J., 1 PROC. NATL. ACAD. SCI. U.S.A. 90:2112-2116(1993).
                                                                                                                                                                                                                                                                                CELL 71:791-801(1992).
                                                                                                                                                                                                                                                                                                          DENG X.-W., MATSUI M., WEI N., WAGNER D., CHU A.M., FELDMANN K.A.,
                                                                                                                                                                                                                                                                                                                           MEDLINE; 93046683
                                                                                                                                                                                                                                                                                                                                                                                       CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; PLANTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P28990; 1CHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00518; ZINC_FINGER_C3HC4.

    -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 lhselmcpicldmlkntmttkeclhrfcsdcivtalrsgnkecptc 58 | : : |: | :: | : | | | | : | | | | : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 LEAKYLCSACKNILRRPFQA-QCGHRYCSFCLTSILSSGPQNCAAC 72
                                                                                                                                                      TRP-ASP DOMAINS
                                                                                                                                                                                                               INTERACTION WITH COMPONENTS OF THE G PROTEIN SIGNALING PATHWAY.
                                                                                                                                                                                                                               AS A NEGATIVE TRANSCRIPTIONAL REGULATOR CAPABLE OF DIRECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                        PS00518; ZINC FINGER C3HC4. PS00678; G_BETA_REPEATS.
                                                            675 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 32, CREATED)
(REL. 32, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                             76260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39145 MW;
                                                                                                                                                                                                                                                                                                                                        TISSUE=WHOLE SEEDLING;
               Score 135; DB 2;
Pred. No. 1.40e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141; DB 7;
Pred. No. 1.69e-06;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR LOCALIZATION SIGNAL (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                             2370819 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 716288 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
16;
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                            Length 675;
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 Indels
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Gaps
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28 LEAKYLCSACKNILRRPFQAQCGHRYCSFCLTSILSSGPQNCAAC 72

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        3385
                                                                                                                      RESULT
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Best Local Similarity 28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC-FINGER; METAL-BINDING; DNA-BINDING; RE
T ZN FING 317 339 C2H2-TYPE.
T ZN FING 317 339 C2H2-TYPE.
T ZN FING 345 367 C2H2-TYPE.
T ZN FING 401 423 C2H2-TYPE.
T ZN FING 429 451 C2H2-TYPE.
T ZN FING 429 451 C2H2-TYPE.
T ZN FING 485 507 C2H2-TYPE.
T ZN FING 513 535 C2H2-TYPE.
T ZN FING 513 535 C2H2-TYPE.
T ZN FING 540 563 C2H2-TYPE.
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T ZN FING 540 563 C2H2-TYPE.
T ZN FING 541 563 C2H2-TYPE.
T ZN FING 569 591 C2H2-TYPE.
T ZN FING 569 591 C2H2-TYPE.
T ZN FING 625 647 C2H2-TYPE.
T ZN FING 625 647 C2H2-TYPE.
T ZN FING 625 647 C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
  01-FEB-1994
01-FEB-1994
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01-NOV-1990
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P18723;
                                                         YNN1 CAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-339 FROM N.A. MEDLINE; 89345612. KNOCHEL W., POTING A., KOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00028; ZINC_FINGER_C2H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P07248; 1ARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GASTRULA ZINC FINGER PROTEIN XLCGF48.2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S06573; S06573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. MOL. BIOL. 208:639-659(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIETFELD W., EL-BARADI T., MENTZEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOUWMEESTER T., PIELER T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; F33282; F33282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M25871; M25871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POETING A., KNOECHEL W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90040698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROC. NATL. ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XENOPUS LAEVIS (AFRICAN CLAWED FROG).
                                                                                                                                                                                                                                                       425 gee-pfvcsecgksfaqspqldlhmrihtgek-pfscsdcgkcftqradlnvhrrt 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 312-647 FROM N.A.
                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                                                                             365 rnhtgekpfscsecgkcfkwrsllikhhkthtgdksftcadcgkcfkkfsrltehrkcht 424
                                                                                                                                                                                                                                                                                                                                 97
                                                                                          CAEEL
                                                                                                                                                                                                        EQECPKRSLSCQHCRAPCSHVDLEVHYEVCPKFPLTCDGCGKKKIPRETFQDHVRA
                                                                                                                                                                                                                                                                                                                         RREVESLPAVCPNDG-C-TWKGTLKEYESCHEGLCPFLLTECPAC-KGLVRLSE-KEHHT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ყ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL. 16, LAST SEQUENCE UPDATE)
(REL. 30, LAST ANNOTATION UPDATE)
(REL. 28, CREATED)
(REL. 28, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOSTER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 126; DB 9;
Pred. No. 3.04e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86:6097-6100(1989)
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2104456 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EL BARADI T., NIETFELD W.,
                                                                                          160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIELER T.,
                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               6:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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Dec 10 06:50 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
HYPOTHETICAL 18.7 KD PROTEIN T02C1.1 IN CHROMOSOME III. US-08-446-915-4.rsp

EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA. CAENORHABDITIS ELEGANS.

T02C1.1.

STRAIN=BRISTOL N2; MEDLINE; 94150718. SEQUENCE FROM N.A.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONNFIELD J., BURTON J., CONNELL M., COPSET J., COVERS J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GRADNER A., GREEN P., HAWKINS T., HILLIER L.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATRELILE P., LICHTNING J., LLOYD C., MORTINORE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN æ

SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,

NATURE 368:32-38(1994). WOHLDMAN P.;

-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

EMBL; Z19156; Z19156.

WORMPEP; T02C1.1; CE00312. PIR; S28290; S28290.

PROSITE; PS00518; ZINC FINGER C3HC4. HYPOTHETICAL PROTEIN; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN

SEQUENCE ZN FING 160 AA; 18675 MW; 132007 CN; C3HC4-TYPE

B Matches Best Local Similarity 31.8%; Query Match 14; Conservative Score 120; DB 9; Pred. No. 2.21e-03; 12; Mismatches 17; Length 160; Indels 1; Gaps ;

Ş 29 EAKYLCSACKNILRRPFQAQCGHRYCSFCLTSILSSGPQNCAAC STANDARD; PRT; 227 ₽ 72

RESULT RE 01-JUL-1989 01-NOV-1995 TPMS HUMAN P10469; 01-JUL-1989 EUKARYOTA; METAZOA; HOMO SAPIENS (HUMAN). TPM1 OR TMSA TROPOMYOSIN ALPHA (REL. (REL. L. 11, CREATED)
L. 11, LAST SEQUENCE UPDATE)
L. 32, LAST ANNOTATION UPDATE)
HA CHAIN, SMOOTH MUSCLE (FRAGME) CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; (FRAGMENT).

EUTHERIA; PRIMATES

TISSUE=LIVER; SEQUENCE FROM N.A.

MEDLINE; 88333013.

COLOTE S., WIDADA J.S., FERRAZ C., BONHOMME F., MARTI J.,

LIAUTARD J.-P.;

J. MOL. EVOL. 27:1228-235(1988).

-!- FUNCTION: THE FUNCTION OF TROPOMYOSIN IN SMOOTH MUSCLE AND

MUSCLE CELLS IS NOT CLEAR.

-!- SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.

-!- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQ

EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY. THE SEQUENCE

-!- ALTERNATIVE PRODUCTS: THE VARIOUS TROPOMYOSIN ISOFORMS ARE

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PACE TO THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUTREAL P.A., LIU Q., SHATTUCK-EIDENS D., COCHRAN C., HARSHMAN TAVTIGIAN S., BENNETT L.M., HAUGEN-STRANO A., SWENSEN J., MIKI EDDINGTON K., MCCLURE M., FRYE C., WEAVER-FELHAUS J., DING W., GHOLAMI Z., SOEDERKVIST P., TERRY L., JHANWAR S., BERCHUK A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TANTIGIAN S., LIU Q., COCHRAN C., BENNETT L.M., DING W., BELL R., ROSENTIAL J., HUSSEY C., TRAN T., MCCLURE M., FRYE C., HATTIER T., PHELES R., HANGEN-STRANO A., KATCHER H., YAKUMO K., GHOLAMI Z., SHAFFER D., STONE S., BAYER S., WRAY C., BOCDEN R., DAYANANTH P., SHAFFER D., TONIN P., NAROD S., BRISTOW P.K., NORRIS F.H., HELVERING L., WORRISON P., ROSTECK P., LAI M., BARRETT J.C., LEWIS C., NEUHAUSEN S., CANNON ALDERING TO THE CONTROL OF THE PROPERTY OF THE P
                                                                                                                                                                            CASTILLA L.H., COUCH F.J., ERDOS M.R., HOSKINS K.F., CALZONE K., GARBER J.E., BOYD J., LUBIN M.B., DESHANO M.L., BRODY L.C., COLLINS F.S., WEBER B.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P38398;
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MIM; 191010; 11TH EDITION.

PROSITE; PS00326; TROPOMYOSIN.

MUSCLE PROTEIN; COILED COIL; REPEAT; ALTERNATIVE SPLICING.

NON TER 1 1
                                                                                                                                                                                                                                                               CASTILLA L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        KAMB A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1994
VARIANTS BC G-61, AND VARIANTS R-356; G-1038; N-1040; R-1183 & G-1613. FRIEDMAN L.S., OSTERMEYER E.A., SZABO C.I., DOWD P., LYNCH E.D.,
                                                                                                                                                                                                                                                                                                      VARIANTS BC GLY-64 AND GLY-1443,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CANNON-ALBRIGHT L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIKI Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 95025896.
                                                                                                                                         NAT. GENET. 8:387-391(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGLEHART J.D., MARKS J., BALLINGER D.G., BARRETT J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS LEU-1637; GLU-1708 AND ARG-1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIENCE 266:66-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X12369; X12369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 GIKDLAMADLEQKVSELE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 efaersvtkleksiddle 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRCQILEQKIATFENIVCVLNREVERVAVTAEACS-RQHRLDQDKIEALSNKVQQLERSI 328
                                                                                                                                                                                                                                                                                                                                                                                         , WISEMAN R.;
266:120-122(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWENSEN J., SHATTUCK-EIDENS D., FUTREAL P.A., HARSHMAN K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95025878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REL. 31, (REL. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GODLGAR D., WISEMAN R., KAMB A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND VARIANT ARG-1775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26576 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225728 CN;
                                                                                                                                                                                                                                                                                                          AND VARIANTS ALA-772 AND ASN-1040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1863 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKOLNICK M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKOLNICK M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                    OMPA_THEMA
Q01969;
                                                              EMBO J. 11:4369-4378(1992).
-!- FUNCTION: LINKS THE OUTER MEMBRANE TO THE INNER MEMBRANE. LONG
FIBROUS PROTEIN THAT COULD SERVE TO SEPARATE THE TWO MEMBRANES
                                                                                                                                                                                                                01-0CT-1994 (REL. 30, LAST ANNOTATION U OUTER MEMBRANE PROTEIN ALPHA PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
VARIANT
VARIANT
VARIANT
          EMBL; X68276; X68276.
                         -!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: CONTAINS A COPY OF THE S-LAYER HOMOLOGY (SLH) DOMAIN.
                                                                                                       ENGEL A.M., CEJKA Z., LUPAS A., LOTTSPEICH F., BAUMEISTER W.;
                                                                                                                                   STRAIN=MSB8 / DSM 3109;
                                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                                         THERMOTOGA MARITIMA.
PROKARYOTA; NOT YET
                                                                                                                                                                                                     OMP-ALPHA.
                                                                                                                                                                                                                                           01-JUL-1993
                                                                                                                                                                                                                                                          01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZN_FING
                                                                                                                      MEDLINE; 93049187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN; DISEASE MUTATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DISEASE: BREAST CANCER (BC) IS AN EXTREMELY COMMON MALIGNANCY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAT. GENET. 8:399-404(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROWELL S.E., KING M.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYMORPHISM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 113705; 11TH EDITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U14680; U14680.

    !- SUBCELLULAR LOCATION: OUTER MEMBRANE.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00518; ZINC_FINGER_C3HC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY:

    -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    !- FUNCTION: NOT KNOWN, MAY REGULATE GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                        Match 3.2%;
Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                         31 KYL-CSACKNILRRPFQAQCGHRYCSFCLTSILS--SGPQNCAAC
                                                                                                                                                                                                                                                                                                                                                               20 kilecpiclelikepvstkcdhifckfcmlkllnqkkgpsqcplc
S28022; S28022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF INHERITED BREAST AND OVARIAN CANCER (BOC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESPONSIBLE FOR 45% OF INHERITED BREAST CANCER AND MORE THAN 80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONSET BREAST CANCER. MUTATIONS IN BRCA1 ARE THOUGHT TO BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENT OF THE DISEASE, AND THIS LINK IS STRIKING FOR EARLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY HISTORY HAS BEEN IDENTIFIED AS MAJOR CONTRIBUTOR TO RISK OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFFECTING ONE IN EIGHT WOMEN DURING THEIR LIFETIME. A POSITIVE
                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1443
1613
1637
1708
1775
                                                                                                                                                                                                                                                          (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1040
                                                                                                                                                                                                                                           (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
61
64
356
772
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-ONCOGENE
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                            26, CREATED)
26, LAST SEQUENCE UPDATE)
30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
61
64
356
372
1038
1040
1183
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1637
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                                                                                                                                               AND PARTIAL SEQUENCE
                                                                                                                                                                          CLASSIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                   207720
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C -> G (IN BREAST CANCER).
C -> G (IN BREAST CANCER).
Q -> R.
Q -> R.
V -> A.
E -> G.
S -> N.
K -> R.
R -> G (IN BREAST CANCER).
S -> G.
S -> G.
S -> G.
S -> G.
N.
R -> G (IN BREAST CANCER).
S -> G.
P -> L (IN BREAST CANCER).
A -> E (IN BREAST CANCER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                         Score 120; DB 1;
Pred. No. 2.21e-03;
                                                                                                                                                                                                                                                                                                                                                                                            11; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C3HC4-TYPE
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16213725 CN;
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                                                                                                                                                                                                                                                                                     400
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1863;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                  64
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                                                                                              Query Match 3.1%;
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.1%;
Best Local Similarity 20.6%;
                                                                                                                                                                                            ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=C1-T10-34A; MEDLINE; 93241158. TOMITA H., SOSHI T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UVS2 NEUCR
P33288;
01-FEB-1994
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
CHAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                PIR; S34825; S34825.

PROSITE; PS00518; ZINC FINGER C3HC4.

PROSITE; PS00518; DNA-BIDING; DNA DAMAGE; DNA REPAIR; NUCLEAR PROTEIN.

ZINC-FING 34 71 C3HC4-TYPE.

ZN_FING 189 209 C2HC-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UVS-2.
                                                                                                                                                                                                                                                                                                                                                          TOMITA H., SOSHI T., INOUE H.;
MOL. GEN. GENET. 238:225-233(1993).
-!- FUNCTION: MAY BE AN ACTIVATOR THAT FUNCTIONS IN THE TRANSCRIPTION
OF DNA REPAIR GENES.
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; FUNGI; ASCOMYCOTINA; PYRENOMYCETES; SORDARIALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UVS-2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01072; SLH DOMAIN. OUTER MEMBRANE; SIGNAL; COILE
                                                                                                                                                                                                                                                                                                                                            EMBL; D11458; D11458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEUROSPORA CRASSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 ALSNKVQ-QLERSIGLKDLAMADLEQKVSELEVSTYD 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 avkeeiemefdkeisInrevvnniglklgnls-rdye 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::| | | | | :| :: | | | | :| 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 gasgdlaqvvgnlsdkymaleekvngitgildtlasqigttqanltetere--1-lekid 137
  28
                         28 veqafrchvckdfydspmltscnhtfcslcirrclsvds-kcplc 71 : | : | : | : : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
LEAKYLCSACKNILRRPFQAQCGHRYCSFCLTSILSSGPQNCAAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                            189 209 C2HC-TYPE.
501 AA; 54830 MW; 1166525 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REL. 28, CREATED)
(REL. 28, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 AA;
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400
84
379
400
350
232
275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 114; DB 8; I
Pred. No. 1.51e-02;
11; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 113; DB 6;
Pred. No. 2.07e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OUTER MEMBRANE PROTEIN ALPHA.
SLH.
COILED COIL.
MEMBRANE ANCHOR (POTENTIAL).
3 X 25 AA APPROXIMATE REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                19;
                                                                                                                                           Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 400;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                           1;
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                                                                                           Gaps
                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
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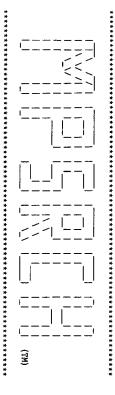
Search completed: Tue Dec 10 07:06:57 1996

Dec 10 06:50 US-08:446:915:4.rsp

6

Job time : 28 secs

US-08-446-915-4\_rag



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Dec 10 07:08:41 1996; MasPar time 10.68 Seconds 446.743 Million cell updates/sec

Run on:

Description: Perfect Score: Title: >US-08-446-915-4 (1-501) from US08446915.pep 3702

Sequence: 1 MAAASVTSPGSLELLQPGFS......NSYVRDDAIFIKAIVDLTGL 501

Scoring table: PAM 150 Gap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16

Statistics: Mean 35.625; Variance 156.291; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	DB	ID	Description	Pred. No.
1	3700	1	i	15	R90578	Mouse TRAF2.	0.00e+00
2	972			15	R90577	Mouse TRAF1.	3.96e-79
ω	131			16	R91212	RIN1 zinc finger doma	5.64e-02
4	120			16	R91208	BRCA1, breast and ova	3.81e-01
5	120			15	R76641	BRCA1 protein.	3.81e-01
o م	111			16	R91210	BRCAl polypeptide zin	1.74e+00
7	99			_	P94369	Fusion protein conqt.	1.24e+01
80	101			15	R89145	Chondroitinase AC.	9.00e+00
9	96	2.6	45	16	R91211	RPT1 zinc finger doma	2.00e+01
10	95			10	R53430	Human/rat chimeric ci	
=	95			10	R53428	Human/rat chimeric ci	
12	95			5	753230		

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	3
90	ä	89	88	88	88	88	88	88	88	88	88	88	88	89	88	88	88	94	91	94	94	94	94	92	92	97	96	97	97	97	98	96
2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.6	2.6	2.6	2.6	2.6	2.6	2.6
3685	173	775	673	200	200	200	200	200	200	200	200	200	200	200	192	187	161	3084	1427	908	870	854	594	462	263	2482	1093		816	576	475	365
_	7	·		14	10	13	7	10	7	w	Ξ	10	σ		6	7	7	2	2	12	12	12	9	_		14	œ	12	12	12	w	-
₽90290	1140/3	P50121	R06552	R83966	R53425	R70146	R37819	R53432	R34431	R13960	R58303	R53424	R31950	R06234	R32856	R37705	R37707	P94758	R10534	R66053	R66051	R66052	R34936	R05766	R03348	R72826	R42818	R66930	R66931	R66929	R15148	P91461
Human Duchenne muscul	Polypeptide with IGE	Sequence of a polypep	Human 5-lipoxygenase	Ciliary neurotrophic	Human/rat chimeric ci	Human CNTF.	Sequence of human cil	Human/rat chimeric ci	Sequence of human cil	Human CNTF.	Human ciliary neutrop	Human/rat chimeric ci	Sequence of human cil	Human sciatic nerve c	Sequence of neurotrop	Deltal4 hCNTF.	N-terminal delta14/C-	Sequence of mouse lam	Human 160kD mediator			Human NMDA receptor s	CENP-B.	Portion of peptide an	VP2 sequence for HRV	Human mitosin.	TMF.	AMML chromosome inv(1	AMML chromosome inv(1	AMML chromosome inv(1	\ autoantig	Rpt-1 clone cDNA inse
5.10e+01	6.92e+U1		6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	5.94e+01	6.92e+01	6.92e+01	6.92e+01	2.74e+01	4.37e+01	2.74e+01	2.74e+01	2.74e+01	2.74e+01	3.74e+01	3.74e+01	1.71e+01	2.00e+01	1.71e+01	1.71e+01	1.71e+01	1.46e+01	2.00e+01

## ALI GNMENTS

RESULT

R90578 standard; Protein; 501 AA. R90578;

8	PS	PT:	P.	DR	1	Id	PA	PR	PR	PR	ΡF	PD	PN	FT	FT	FΤ	ΤŦ	Ŧ	20	Ž	Ž.	DE	DT
Mouse tumour necrosis factor receptor associated factor 2 (TRAF2)	Claim 8; Page 75-76; 116pp; English.	in mediation of biological activities of TNF and CD40 ligands	Fumour pectosis factor (TNF) recentor-sessociated factors - involved	N-PSDB; T12262.	WP1; 96-049310/05.	Goeddel DV, Rothe M;	(GETH ) GENENTECH INC.	22-MAY-1995; US-446915.	28-OCT-1994; US-331394.	27-MAY-1994; US-250858.	25-MAY-1995; U06639.	07-DEC-1995.	WO9533051-A1.	/label= Leucine_zipper_region	Region 275351	/label= TRAF_domain	Domain 272501	Key Location/Qualifiers	Mus musculus.	TNF; CD40.	<pre>TRAF2; tumour necrosis factor receptor associated factor 2;</pre>	Mouse TRAF2.	09-APR-1996 (first entry)

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Ş 밁 Ş 밁 Ş Ş ð 日 Ş 문 S 문 Ş ននននននននន S 밁 밁 문 문 RESU Query Match 99.9%; Best Local Similarity 99.8%; Matches 09-APR-1996 R90577 standard; R90577; It is used to identify inhibitors of activities of TNF-R2, CD40 and/or LMP1 oncogene, e.g. for treratment of endotoxic (septic) activities. Recombinant TRAF2 is obtd. by expression in host cells of a cDNA clone (T12262) isolated using a yeast two-hybrid assay. TRAF1; tumour necrosis factor receptor associated Mouse TRAF1. Sequence shock and rheumatoid arthritis. (R90578) is a new factor capable of specific association with the intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40, and is involved in the mediation of TNF and CD40 ligand biological /label= TRAF\_domain Region 183..259 Mus musculus. TNF; CD40. activities. 481 481 421 421 361 301 301 241 241 (R90578) is a 361 181 181 121 121 61 2 l maaasvtspgslellqpgfsktllgtrleakylcsacknilrrpfqaqcghrycsfclts eacsrqhrldqdkiealsnkvqqlersiglkdlamadleqkvselevstydgvfiwkisd knsyvrddaifikaivdltgl 501 ftrkrqeavagrtpaifspafytsrygykmclrvylngdgtgrgthlslffvvmkgpnda vcpkfpltcdgcgkkkipretfqdhvracskcrvlcrfhtvgcsemvetenlqdhelqrl yescheglcpflltecpackglvrlsekehhteqecpkrslscqhcrapcshvdlevhye ilssgpqdcaacvyeglyeegisilesssafpdnaarreveslpavcpndgctwkgtlke KNSYVRDDAIFIKAIVDLTGL FTRKRQEAVAGRTP A I FSP AFYTSRYGYKMCLRVY LNGDGTGRGTHLS LF FVVMKGPNDA EACSRQHRLDQDKIEALSNKVQQLERSIGLKDLAMADLEQKVSELEVSTYDGVFIWKISD REHLALLLSSFLEAQASPGTLNQVGPELLQRCQILEQKIATFENIVCVLNREVERVAVTA rehlalllssfleaqaspgtlnqvgpellqrcqileqkiatfenivcvlnrevervavta VCPKFPLTCDGCGKKKIPRETFQDHVRACSKCRVLCRFHTVGCSEMVETENLQDHELQRL YESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHCRAPCSHVDLEVHYE ILSSGPQNCAACVYEGLYEEGISILESSSAFPDNAARREVESLPAVCPNDGCTWKGTLKE 120 MAAASVTSPGSLELLQPGFSKTLLGTRLEAKYLCSACKNILRRPFQAQCGHRYCSFCLTS 60 500; 501 Recombinant TRAF2 is obtd. Conservative (first entry) ž Location/Qualifiers 180..409 Protein; 409 501 Score 3700; DB 15; Pred. No. 0.00e+00; B Mismatches 0 Length Indels 501; 0; Gaps 420 240 120 480 420 360 360 300 240 180 180 60 0

> Dec 10 06:53 US-08-446-915-4.rag

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Best Local Similarity 54.0%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-1995; U06639.
27-MAY-1994; US-250858.
28-OCT-1994; US-331394.
22-MAY-1995; US-446915.
                                                                                                                                                                                                                                                                                                                                                                                 of a cDNA clone (T12261) isolated from murine interleukin-2-dependent cytotoxic T-cell line CT6. It is used to identify inhibitors of activities of TMF-R2, CD40 and/or LMP1 oncogene, e.g. for treratment of endotoxic (septic) shock and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor (TNF) receptor-associated factors - involved in mediation of biological activities of TNF and CD40 ligands Claim 8; Page 71-72; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goeddel DV, Rothe WPI; 96-049310/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse tumour necrosis factor receptor associated factor 1 (TRAF1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T12261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and is involved in the mediation of TNF and CD40 ligand biologica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (R90577) is a new factor capable of specific association with the intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09533051-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
455
                                                                                                                                                                                                                                   183 leeklrvfanivavlnkeveashlalaasihqsqldrehlisleqrvvelqqtlaqkdqv 242
                                                                    363 sfqrpqsetnvasgcplffplsklqspkhayvkddtmflkcivd
                                                                                                                                             335
                                                                                                                                                            243 lgklehslrlmeeasfdgtflwkitnvtkrchesvcgrtvslfspafytakygyklclrl 302 :: ||: : :| ::|| |:||:||:||:||:
                                                                                                                                                                                                                 275 LEQKIATFENIVCVLNREVERVAVTAEACSRQHRLDQDKIEALSNKVQQLERSIGLKDLA 334
SFQRPVSDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD
                                                                                                                                             MADLEQKVSELEVSTYDGVF IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRV
                                                                                                                                                                                                                                                                                                                                                                   409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant TRAF1 is obtd. by expression in host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rothe M;
                                                                                                                                                                                                                                                                                        Score
Pred.
61; M
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                           972; DB 15;
No. 3.96e-79;
                                                                                                                                                                                                                                                                                          41; Indels
                                                                                                                                                                                                                                                                                                                         Length
497
                                  406
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                                                                       454
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Not specified.

W09605307-A2.

22-FEB-1996.

11-AUG-1995; U1

12-AUG-1994; U2

02-SEP-1994; U2

16-SEP-1994; U2

16-SEP-1994; U2

29-NOV-1994; U2

24-MAR-1995; U2

07-JUN-1995; U2
                                                                                                                                                                 LT 3
R91212 :
R91212;
                                                                                                                                                    05-JUN-1996 (first entry)
                                                                                                              prognosis.
                                                                                                                        susceptibility
                                                                                                                                           RIN1 zinc finger domain.
                                                                                                                                 BRCA1; breast cancer; ovary cancer; predisposing gene;
                                                                                                                                                                         standard; Peptide; 41
        U10203.

US-289221.

US-300266.

US-308104.

US-348824.

US-409305.

US-488011.
US-483554
                                                                                                                       gene; protein replacement therapy; diagnosis;
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Region

/label= Leucine\_zipper\_region

US-08-446-915-4.rag

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Best Local Similarity 35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                      12-AUG-1994; US-289221.
02-8EP-1994; US-300266.
16-SEP-1994; US-308104.
29-NOV-1994; US-348824.
24-MAR-1995; US-409305.
07-JUN-1995; US-488011.
07-JUN-1995; US-483554.
07-JUN-1995; US-487002.
Claim 1; Page 117-124; 190pp; English.
The BRCA1 polypeptide (R91208) is the product of the human BRCA1
                                prods. for diagnosis, prognosis and therapy of cancers,
breast and ovarian cancers
                                                                                                                                                            (MYRI-)
(UTAH )
(USSH )
                                                                                                                                                                                                                                                                                                                                                                                                            susceptibility gene; protein replacement therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                         BRCA1; breast and ovarian cancer predisposing gene product. BRCA1; breast cancer; ovary cancer; predisposing gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R91208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R91208 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (R91212) a DNA-binding protein that includes a RING-finger motif related to the zinc finger, and RFPI (R91213) a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A sequence (R91210) near the amino terminus of the human BRCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prods. for diagnosis, prognosis
breast and ovarian cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human cancer predisposing gene, BRCA1 - used to develop prods. for diagnosis, prognosis and therapy of cancers, partic.
                                                                                                             Wiseman RW;
                                                                                                                                             Futreal AP,
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                               prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription factor that is the N-terminal domain of the RET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            negative regulator of the interleukin-2 receptor in mouse, RIN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide (R91208) shows considerable homology to zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 173; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UTAH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995; US-487002.
                                                              New isolated human cancer predisposing gene, BRCAl - used to develop
                                                                              N-PSDB; T18310.
                                                                                              WPI; 96-139703/14.
                                                                                                                            Shattuck-Eidens DM,
                                                                                                                                                                                                                                                                                                                                                                  WO9605307-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains, including RPT1 (R91211) a protein that appears to be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 96-139703/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wiseman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Futreal AP,
                                                                                                                                                                                                                                                                                                                                  11-AUG-1995; U10203
                                                                                                                                                                                                                                                                                                                                                  22-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MYRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 cpicldmlkntmttkeclhrfcsdcivtalrsgnkecptc 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSACKNILRRPFQA-QCGHRYCSFCLTSILSSGPQNCAAC 72
                                                                                                                                                      UNIV UTAH RES FOUND.
US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                       MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 AA;
                                                                                                                                            Goldgar DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldgar DE, Harshman KD, Kamb A, Miki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 1863 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r DE, Harshman KD, Kamb A, Miki Y;
Skolnick MH, Swenson J, Tavtigian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 131; DB 16;
Pred. No. 5.64e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                              partic.
                                                                                                                            ,VS
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RESULT
ID R9
AC R9
DT 05
DE BE

05-JUN-1996 (first entry)

BRCAl polypeptide zinc finger domain. BRCAl; breast cancer; ovary cancer; predisposing gene;

R91210

standard; Peptide; 41

R91210;

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RESULTION AND ACCORD TO THE CONTROL OF THE CONTROL 
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                                                                                                                                              Matches
                                                                                                                                                                        Query Match 3.2%;
Best Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.2%;
Best Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The BRCAl gene was isolated from a human cDNA library of an adult female normal breast tissue. The BRCAl protein gene can be used in a method for gene therapy of breast cancer in a patient by ligating the gene with a promoter capable of inducing gene expression into a virus vector (preferably the Moloney murine leukemia retro virus).
                                                                                                                                                                                                                                                                                                                                                    malignant effusions. Since the BRCAl gene is a negative growth regultor in human breast cells, in-situ expression of the BRCAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRCA1 gene in therapy of breast cancer. Claim 50; Page 91-96; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thompson ME; WPI; 95-269208/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRCAl; breast cancer; diagnosis; prognosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRCA1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R76641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R76641 standard; Protein; 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ovarian cancer, can also be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes, associated in humans with a predisposition to breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene (T18310). It can be obtd. by insertion of BRCA1 DNA into
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                       protein will result in inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                           Vector expressing BRCAl is then infused into solid tumours or into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by identifying differentially expressed marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection, diagnosis and treatment of pre-invasive breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q93027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holt JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-1994; US-182961.
17-JAN-1995; US-373799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9519369-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as immunogens for the prodn. of antibodies, or to screen therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector and expression in host cells; products of mutated BRCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVA-) UNIV VANDERBILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-1995; U00608
31 KYL-CSACKNILRRPFQAQCGHRYCSFCLTSILS--SGPQNCAAC
                                                                20 kilecpiclelikepvstkcdhifckfcmlkllnqkkgpsqcplc 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 KYL-CSACKNILRRPFQAQCGHRYCSFCLTSILS--SGPQNCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 kilecpiclelikepvstkcdhifckfcmlkllnqkkgpsqcplc
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                                                                                                                                              15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jensen RA, Obermiller PS,
                                                                                                                                                                                                                                                                                      1863 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1863 AA;
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                        Score 120; DB 15;
Pred. No. 3.81e-01;
11; Mismatches 16
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Pred. No. 3.81e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
                                                                                                                                              Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                of tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRCAl polypeptides are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes,
                                                                                                                                                                                                            Length 1863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robinson-Benion CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
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                                                                                                                                           Gaps
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Best Local Similarity 34.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-1994; US-348824.
24-MAR-1995; US-409305.
07-JUN-1995; US-488011.
07-JUN-1995; US-483554.
             N-PSDB; N91214. Protein derived from parasitic nematode species protective immunity against nematode parasites of Claim 5; page 40; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide (R91208) shows considerable homology to zinc finger domains, including RPT1 (R91211) a protein that appears to be a negative regulator of the interleukin-2 receptor in mouse, RNN1 (R91212) a DNA-binding protein that includes a RING-finger motif related to the zinc finger, and RFP1 (R91213) a putative transcription factor that is the N-terminal domain of the RET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MYRI-)
(UTAH )
(USSH )
                                                                                                       06-JUL-1988; AU0239.
07-JUL-1987; AU-002940.
(BIOT-) Biotechn Austr Pt, (CSIR) Commonwealth Sci and Ind Res Orgn.
Cobon GS, Austen RA, O'Donnell IJ, Frenkel MJ, Kennedy WPK, Savin KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oncogene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Page 172; 190pp; English.
A sequence (R91210) near the amino terminus of the human BRCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
Futreal AP, Goldgar DE, Harshman KD, Kamb A, Miki Y;
Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human cancer predisposing gene, BRCA1 - used to develop prods. for diagnosis, prognosis and therapy of cancers, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wiseman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-1994; US-289221.
02-SEP-1994; US-300266.
16-SEP-1994; US-308104.
                                                                              WPI; 89-039628/05.
                                                                                              Wagland BM;
                                                                                                                                                                                          WO8900163-A.
                                                                                                                                                                                                      Trichostrongylus colubriformis.
                                                                                                                                                                                                                     Fusion protein congt. 41kD protein of T. colubriformis. Parasitic nematode; 41kD protein; fusion protein.
                                                                                                                                                                                                                                                                                      P94369 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast and ovarian cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 96-139703/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995; US-487002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                susceptibility
The sequence encodes a molecule which is only 4AAs shorter than mature H.
                                                                                                                                                                         2-JAN-1989.
                                                                                                                                                                                                                                                         13-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9605307-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prognosis.
                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                     CSACKNILRRPFQAQCGHRYCSFCLTSILS--SGPQNCAAC 72
                                                                                                                                                                                                                                                                                                                                                                                  cpiclei-kepvstkcdhifckfcmlkllnqkkgpsqcplc 40
                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene;
                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein replacement therapy; diagnosis;
                                                                                                                                                                                                                                                                                        252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 111; DB 16;
Pred. No. 1.74e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 41;
                               used to
man and
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                animals.
                                              provide
                                                                                                                                                                                                                                                                                                                                                                                                                  Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  ?;
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M. B. Q.	38888888	CC CC PT	PD PF PR PA PI PI DR	PN FT	Qy RESULT ID R AC R DT 2 DT 2 C KW C	Db Db	Qu Be Ma Db	នឧឧឧឧឧ
Query Match 2.7%; Score 101; DB 15; Length 700; Best Local Similarity 31.9%; Pred. No. 9.00e+00; Matches 22; Conservative 17; Mismatches 23; Indels 7; Gaps 5;	mol.wis. of 77,169 and 53,563, respectively, can be obtd. by purification from F. heparinum cells or by expression of the encoding genes (see T10316 and T10317) in host cells. They are useful as tools in determining the role of chondroitin sulphates in modulating cellular events, and can also be used to develop therapeutic reagents.	AC and chondroitinanhromatography to franhromatography to frankrish homatographe AC (R89145) capable of degrading capable capa	U08560. U08-277247. TECHNOLOGIES R & D I Fink D, Gu K, Lali immermann J; 4/10.	te. arinum. cation/Qualifiers .23 e e 700	342 VSELE 346  ULT 8 R89145 standard; Protein; 700 AA. R89145; 22-APR-1996 (first entry) Chondroitinase AC; chondroitinase B; chondroitin lyase;	162 eeeltvvgnnlkslevseekalqredsye-eqirtisarlkeaetraefaersvhklqke 220	Query Match 2.7%; Score 99; DB 1; Length 252; Best Local Similarity 23.2%; Pred. No. 1.24e+01; Matches 29; Conservative 35; Mismatches 55; Indels 6; Gaps 5;  b 102 vdvdedrcaeletklreaqallheteskseevarklamveadleraeeraeagenkivel 161   : : :     :       :       :   :       :	contortus 41 kD protein. The 6 AAs on the N-terminus are derived from beta-galactosidase. Recombinant organisms contg. DNA encoding the protein can be used to produce polypeptide which is capable of protecting guinea pigs against parasitism from T. colubriformis. See also P94260, and P94366-P94368.

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                                                RESULT
                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1994; US-300266.

16-SEP-1994; US-308104.

29-NOV-1994; US-348824.

24-MAR-1995; US-409305.

07-UUN-1995; US-488011.

07-UUN-1995; US-483554.

07-UUN-1995; US-487002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS 4P.
WO9605307-A2.
22-FEB-1996.
11-AUG-1995; U10203.
12-AUG-1994; US-289221.
                                                                                                                                                                                                                                               A sequence (R91210) near the amino terminus of the human BRCAl polypeptide (R91208) shows considerable homology to zinc finger domains, including RPT1 (R91211) a protein that appears to be a negative regulator of the interleukin-2 receptor in mouse, RINI (R91212) a DNA-binding protein that includes a RING-finger motif related to the zinc finger, and RFP1 (R91213) a putative transcription factor that is the N-terminal domain of the RET
R53430;
13-DEC-1994 (first entry)
                             R53430 standard; protein; 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MYRI-) MYRIAD GENETICS INC.
(UTAH ) UNIV UTAH RES FOUND.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Futreal AP, Goldgar DE, Harshman KD, Kamb A, Miki Y;
Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPT1 zinc finger domain.

RPT1; BRCAl; breast cancer; ovary cancer; predisposing gene; susceptibility gene; protein replacement therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R91211 standard; Peptide; 45 AA.
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                  oncogene product.
                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 172; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          New isolated human cancer predisposing gene, BRCAl - used to develop prods. for diagnosis, prognosis and therapy of cancers, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R91211;
                                                                                                                                                                                                                                                                                                                                                                             breast and ovarian cancers
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 96-139703/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wiseman RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 LNGDGTGRG 404
                                                                                                                                               2.6%;
Local Similarity 38.5%;
nes 10; Conservat'...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 mdfnvegrg 289
                                                                                             မှု
                                                                                          1 cpiclellkepvsadcnhsfcracit 26
|: | ::|: | |:| |:| |:|
34 CSACKNILRRPFQAQCGHRYCSFCLT 59
                                                                                                                                                                                                                   45 AA;
                                                                                                                                                      Score 96; DB 16; Length 45; Pred. No. 2.00e+01; 7; Mismatches 9; Indels
                                                                                                                                                        0;
                                                                                                                                                        Gaps
                                                                                                                                                        0
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<b>3</b> 8	<pre>Human/rat chimeric ciliary neurotrophic factor RPN222. Human ciliary neurotrophic factor; hCNTF; mutant; variant;</pre>
₹ ₹	receptor binding; enhance; nervous system disorder; treatment; chimeric protein; electrophoretic mobility.
8 8	Chimeric Homo sapiens. Chimeric Rattus sp.
E	
7 7	Misc_difference 53
H .	ifference 67
PN	/note= "Leu is substd. by Met" W09409134-A.
PD	28-APR-1994.
PR	08-0CT-1993; U09649. 09-0CT-1992; US-959284.
PA	(REGE-) REGENERON PHARM INC.
DR PI	Panayotatos N; WPI; 94-151319/18.
PT	fied human
P	ceptor binding and
PS T	Example 1; Page 32; 46pp; English.
S	the same number of
88	similar mass (22.7 kD). On reducing SDS-PAGE gels, however, recombinant bCNTF migrates as a protein of moleut 27.5 kD while rat CNTF
8	tes as expected. The hCNTF also has 4 times lower
38	activity towards chick ciliary ganglion neurons than rat CNTF. The
8 8	than human CNTF. A series of chimeric proteins was prepared in
38	cresp. ra
3 8	sequence (see kbb4zb-kbb4zb). It was found that all variants with
888	CNTF. Human CNTF in which Gln at position 63 is replaced by Arg is
ŞQ	Sequence 200 AA;
Quer	Match 2.6%; Score 95; DB 10; Length 200; Local Similarity 35.6%; Prod. No. 2.34e+01;
Ma Db	Matches 21; Conservative 13; Mismatches 21; Indels 4; Gaps 65 semteaerlgen-lgayrt-fhvllarlledgqvhftpte-g-dfhqaihtlllqvaaf 119
Ş	
RESULT	LT 11 R53428 standard; protein; 200 AA.
3 8	13-DEC-1994 (first entry)
至日	Human/rat chimeric ciliary neurotrophic factor RPN218. Human ciliary neurotrophic factor; hCNTF; mutant; variant;
€	
S	Chimeric Homo sapiens.
S	Chimeric Rattus sp. Key Location/Oualifiers
Ŧ	c_difference
T T	/note= "Thr is substd. by Met" Wisc difference 53
1 13	/note= "Ala is substd. by Val"
F) I	/note= "Met is substd. by Val"
7 7	Misc_difference 63 /mote= "Gin is substd. by Arg"

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US-08-446-915-4 rag

#### Ş 밁 Ş В Best Query Match 2.6%; Best Local Similarity 35.6%; Matches Query Match Matches P91461; 10-MAR-1993 rat CNTF competes for binding to the human or rat receptor better than human CNTF. A series of chimeric proteins was prepared in which part of the human CNTF was replaced by the corresp. rat sequence (see R53423-R53432). It was found that all variants with an arginine residue at position 63 display the mobility of rat CNTF. Human CNTF in which Gln at position 63 is replaced by Arg is cDNA was prepd. from I cells (fibroblast tumour) and 2PK3 (B cell lymphoma). Host was pref. E. coli NRLL -18297. Cysteine residues positions 15, 18, 35, 38, 55, 58, 115 and 118, and histidine residu positions 124 and 127 may be involved in metal finger formation. Positions are given from the methionine (a.a 13 in the sequence g Homo sapiens. W08907652-A. Rpt-1 clone cDNA insert. Regulatory protein T lymphocyte-1; IL-2 receptor; 09-JAN-1990 P91461 Sequence claimed migrates as expected. The hCNTF also has 4 times lower biological Recombinant human and rat CNTF have the same number of amino acids and similar mass (22.7 kD). On reducing SDS-PAGE gels, however, recombinant biological activity. Sequence Claim 20; fig 2; 58pp; English. gene expression of interleukin-2 receptor and of human lymphotrophic Regulatory protein T lymphocyte-1 gene and corresp. protein - increase WPI; 89-263719/36. Cantor HI, Patarca R, Freeman GJ; human lymphotrophic retroviruses; metal fingers. activity towards chick ciliary ganglion neurons than rat CNTF. hCNTF migrates as a protein of mol.wt. 27.5 kD while rat CNTF Example 1; Page 31; 46pp; English. See also N90702 (DANA) Dana-Farber Cancer Institute. 11-FEB-1988; US-154758. 10-FEB-1989; U00550 24-AUG-1989. cetroviruses. 27 cpiclellkepvsadcnhsfcracit 52 |: | :: | |: | |: | |: | Match 2.6%; Local Similarity 38.5%; 34 CSACKNILRRPFQAQCGHRYCSFCLT 59 standard; peptide; 365 10; 365 AA; 200 AA; Conservative Conservative (revised) (first entry) Score 96; DB 1; L Pred. No. 2.00e+01; Score 95; DB 10; Pred. No. 2.34e+01; 13; Mismatches 21; Indels A Mismatches Length 365; Length 200, and histidine residues at Indels sequence given). 4; 0 Gaps The Gaps at 0; 4;

RESULT ID R1

R15148 standard; Protein; 475 AA.

US-08-446-915-4.mg

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RESULT
RESULT
REA
AC AC REA
AC Ş 밁 Best Matches Query Match 26-JUL-1994, U08530. 29-JUL-1993, US-099869. (UNMI) UNIV MICHIGAN. (TEXA) UNIV TEXAS SYSTEM. Peptide /label= MYHll A cDNA library (from human thymus mRNA) in lambda gtll was screened with serum from a patient having systemic lipus erythematosus. Two clones were reactive with sera (from a panel of luss patients) which contd. autoantibodies against 52 kD protein.

Both the cDNA and the protein expressed from it, or portions of it, are useful as diagnostic agents in the identification of patients PCR was performed on total cellular RNA from 5 AMML patients having Novel DNA spanning the pericentric inversion of chromosome for the screening of acute myeloid leukaemia Claim 4; Page 28-30; 78pp; English. R66929 standard; Protein; 576 AA. DNA encoding an Ro-SSA autoantigen - useful for diagnosing auto-immune disorders or presence of auto-antibodies Disclosure; Fig 2; 41pp; English. Frank MB, Itoh K; 07-MAY-1990; US-520270. Homo sapiens. W09117171-A. R15148; N-PSDB; Q84588. Claxton D, Collins FS, Key AMML; 01-SEP-1995 (first entry) having autoantibodies and in the identification and analysis of the structural and functional properties of the autoantigen and N-PSDB; Q14798. WPI; 91-353712/48. Ro/SSA autoantigen. WPI; 95-082178/11. 09-FEB-1995 WO9504067-A. inv(16); CBF-beta; AMML chromosome inv(16) product. Sequence 07-MAY-1991; U03139. Autoantibody; autoantigen; SLE; systemic lupus erythematosus. 14-FEB-1992 'label≃ eptide domo sapiens. application in immunotherapeutic regimens. (OKLA-) OKLAHOMA MED RES FO 4-NOV-1991. 32 / Match 2.6%; Local Similarity 28.2%; CSACKNILRRPFQAQCGHRYCSFCLTSILSSGPQNCAAC cpicldpfvepvsiecghsfcqecisqvgkgggsvcpvc 54 acute myelomonocytic leukemia; chromosome-16; inversion; 6); CBF-beta; CBFB gene; transcription factor; myosin; MYHll; CBFB 11; 475 AA; Conservative (first entry) 165..576 1..164Location/Qualifiers Liu P, Score 98; DB 3; Length 475; Pred. No. 1.46e+01; 10; Mismatches Siciliano MJ; 18; 72 Indels 16 -0; Gaps for

0

pericentric inversion of chromosome-16, M4Eo subtype. Sequencing

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showed the inv(16) fusion to comprise a sequence from the CBFB

gene, encoding a novel transcription factor, and the MYH11 gene, encoding smooth muscle myosin heavy chain. In 3 patients, nt 1-492 of the CBFB gene were fused to nt 1921 of MYH11 (shown in

8888888 Q84588; predicted aa sequence in R66929). Probes based on inv(16)

can be used for diagnosis of AMML.

Sequence 576 AA;

Query Match 2.6%; Best Local Similarity 29.6%; Matches 16; Conservative Score 97; DB 12; Pred. No. 1.71e+01; 20; Mismatches 15; Length 576; Indels <u>υ</u> Gaps

μ

Ş 밁 414 erstagknesargg-lergnke-lrsklhemegavkskfkstiaaleakiagle 465 294 ERVAVTAEACSROHRLDODKIEALSNKVOOLERSIGLK-DLAMADLEOKVSELE 346

Search completed: Tue Dec 10 07:09:39 1996 Job time : 58 secs.

Dec 10 06:49

----<< (MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:04:40 1996; MasPar time 9.40 Seconds  $414.306\ \mathrm{Million}$  cell updates/sec

Tabular output not generated.

>US-08-446-915-2 (1-409) from US08446915.pep

Description: Perfect Score:

Sequence: 1 MASSSAPDENEFQFGCPPAP.....KHAYVKDDTMFLKCIVDTSA 409

Scoring table: PAM 150 Gap 11

81589 seqs, 9523651 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq24

1:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 34.957; Variance 160.267; scale 0.218

Statistics:

## SUMMARIES

etr med gen ce. ce. ane		R78258 R26173	3.5 509 5 R30429 3.4 77 6 R32698	3.5 192 12 R62757	3.8 1427 2 R10534	3.8 870 6 R31348	33.0 501 15 R90578	100.0 409 15	Result Query No. Score Match Length DB ID Description
	<b>-</b>	w w	~ ~	~ 0	1534 Human 160kD mediator	~	_		Description

45	44	43	42	41	40	39	38	37	36	<u>35</u>	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
88	89	88	88	88	88	88	89	88	88	88	88	88	91	90	92	90	91	92	90	92	92	92	95	95	93	93	93	94	100	101	101	101
3.0		3.0				3.0		3.0		3.0		3.0	3.1	3.1	3.1	ω 	ω 1	3.1	3.1	3.1	3.1			•							3.4	3.4
5035	2101	1764	1365	897	885	816	615	435	435	433	239	239	15281	1147	955	648	476	462	394	362	320	235	1618	1618	444	405	405	405	1093	738	738	738
S	œ	_	6	16	12	12	5	2	-	2	2	~	∞	œ	=	16	œ	_	16	œ	_	_	Ξ	5	16	11	11	11	œ	15	5	15
R25450	R47173	P91672	R36780	R92751	R66930	R66931	R74630	P91289	P90992	R08335	R04118	R04117	R44929	R41199	R57365	R94906	R43563	R05766	R94559	R41536	P94366	P94260	R60127	R27205	R86801	R61174	R57498	R57499	R42818	R69850	R69849	R69853
MH mutant porcine rya	e of the inne	Primary amino acid se	KRE5.			AMML chromosome inv(1		Sequence of a segment	Human CD4 antigen	CD4.	Enod2b		T. niveum Cyclosporin	CAI antigen.	K39 polypeptide of Le	RAP-1 radiation prote	Hyaluronan receptor.		Human Gs alpha protei	2 toxi	protein of T.	protein	Human nestin protein		<ol> <li>T. thermophilus gamma</li> </ol>	Corticosteroid bindin	cortico	Human varient cortico		response	response	Ethylene response (ET
7.37e+01	6.35e+01	7.37e+01	7.37e+01	7.37e+01	7.37e+01	7.37e+01	6.35e+01	7.37e+01	7.37e+01	7.37e+01	7.37e+01	7.37e+01	4.71e+01	5.47e+01	4.06e+01	5.47e+01	4.71e+01	4.06e+01	5.47e+01	4.06e+01	4.06e+01	•	•	2.57e+01	3.49e+01		3.49e+01	3.00e+01	1.19e+01	1.02e+01	1.02e+01	1.02e+01

# ALI GNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.0%;
Best Local Similarity 54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activities. Recombinant TRAF2 is obtd. by expression in host cells of a cDNA clone (T12262) isolated using a yeast two-hybrid assay. It is used to identify inhibitors of activities of TNF-R2, CD40
                           was prepared from an appear of the semi-purified lung lavage samples from infected sheep. The semi-purified lung lavage samples from infected sheep. The invention includes the Pol amino acid sequence or any part of it invention includes the Pol amino acid sequence or any part of it invention includes the Pol amino acid sequence or any part of it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R31348 standard; Protein; 870 R31348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in mediation of biological activities of Claim 8; Page 75-76; 116pp; English.
directed against JSRV
                                                                                                                                               adenomatosa in sheep. The complete cDNA sequence of the JSRV genome was prepared from an approx. 8.7kb band of poly-A RNA isolated from
                                                                                                                                                                                                                                                                  Claim 25; Page 39-42; 75pp; French.
                                                                                                                                                                                                                                                                                                     derived proteins, probes and antibodies, diagnosis and in vaccines
                                                                                                                                                                                                                                                                                                                                               New Jaagsiekte Retrovirus and characteristic nucleic acid - also derived proteins, probes and antibodies, useful for in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q35153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 93-020250/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Querat GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-1991; FR-006060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FR2676455-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jaagsiekte retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pulmonary adenomatosa; reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JSRV; epithelial carcinoma; ovine; sheep; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or LMP1 oncogene, e.g. for treratment of endotoxic (septic)
shock and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40, and is involved in the mediation of TNF and CD40 ligand biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse tumour necrosis factor receptor associated factor 2 (TRAF2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor (TNF) receptor-associated factors - in mediation of biological activities of TNF and CD40 ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T12262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 96-049310/05.
                                                                                                                                                                                     JSRV causes epithelial carcinoma in ovine animals, partic. pulmonary adenomatosa in sheep. The complete cDNA sequence of the JSRV genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRM ) INSERM INST NAT SANTE & RECH MED.
Querat GF, Verwoerd D, Vigne R, York D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jaagsiekte retrovirus Pol protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-1991; 006060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (R90578) is a new factor capable of specific association with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 madleqkvselevstydgvfiwkisdftrkrqeavagrtpaifspafytsrygykmclrv 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sfqrpvsdmniasgcplfcpvskmea-knsyvrddaifikaivd 497
||||| |: |:|||||| |:||::: |::||:||::|:| |||
SFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKDQV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGKLEHSLRIMEEASFDGTFIWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCIRL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leqkiatfenivcvlnrevervavtaeacsrqhrldqdkiealsnkvqqlersiglkdla 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 972; DB 15;
Pred. No. 7.66e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factors - involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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US-08-446-915-2 rag

See also R31346-7,

R31349 and Q35153-Q35155.

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Best Local Similarity 24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                               Matches
                                                                                                                                                            Query Match 3.8%;
Best Local Similarity 25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Odink KG, Tarcsay L, Bruggen J, Wiesendanger W, Cerletti N; Sorg C, Dewolf-Peeters C, Delabie J; WPI; 91-038913/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R10534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R10534 standard; Protein; 1427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 160kD mediator of inflammation protein.
Mediator of Imflammation; cytokine; Hodgkin's lymphoma; MRP-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                      glycosylated or acylated and have mol. wt.s of 190 and 140kD,
                                                                                                                                                                                                                                                                                                                                                                                                       conditions. It is prepared by chromatographically purifying an
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 32; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 kD human polypeptide mediator or precursor of inflammation polyclonal or monoclonal antibodies to polypeptide treat and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-1991
                                                                                                                                                                                                                                   respectively.
                                                                                                                                                                                                                                                                         the protein in which the amino and/or hydroxyl
                                                                                                                                                                                                                                                                                            polypeptide fragment from amino acids 878-1427 and derivatives of
                                                                                                                                                                                                                                                                                                             with plasmids encoding MRP-160. The invention also covers the
                                                                                                                                                                                                                                                                                                                               by microorganisms or continuous mammalian cell lines, transformed
                                                                                                                                                                                                                                                                                                                                                epithelial lung cells. Alternatively, the protein can be produced
                                                                                                                                                                                                                                                                                                                                                                                    optionally pre-purified cell extract,
                                                                                                                                                                                                                                                                                                                                                                                                                          The protein is a cytokine used to treat chronic inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnose chronic inflammation and hodgkins lymphoma
                  509 alrvqe-vaelrrrl-esnkpagdvdmslsilqeis 542
                                                                                       451 tkgdletqtklehari-keleqøl-lfektkadklqreledtrvatvseksrimelekdl 508
                                                                                                                                                                                                                                                                                                                                                                     filtrate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-1990; 810481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 prvyntqlvklqtdh-lktlndfqkllgdinwirpyl 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 ELALQHLVKEKLLAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHL-LSLE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 QRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 qlylvhymddillahtdehl-lyqaf-silkqhlslnglviadekiqthfpynylgfsly 244
                                                                        165
LLSLEQRVVELQQTLAQKDQVLGKLEHSLRIMEEAS 257
                                                                      SQEELALQ-HLVKEKLLAQLEEKLRVFANIVAV-LNKEVEASHLA-LAASIHQSQLDREH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 870 AA;
                                                                                                                                                                                                                    1427 AA;
                                                                                                                                                                                                                                                                                                                                                                   stimulated normal human leucocytes or human embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB-015414.
                 = ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 112; DB 6;
Pred. No. 1.77e+00;
                                                                                                                                                            Score 113; DB 2; Length 1427; Pred. No. 1.51e+00;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                      cell supernatant or cell
                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 870;
                                                                                                                                                                                                                                                                         functions are
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                           7
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Ħ RESULT

R62656 standard; Protein; 383 AA

Ş В Ş 밁 Query Match 3.6%; Best Local Similarity 27.1%; Matches a protein involved with regulating anthocyanin synthesis in Maize. Comparison of the pH6 and R(S) sequences over the 54 AA helix-loophelix region detected 57% AA identity. Outside this region only 19% Petunia Ph gene and constructs containing it - for alteration of vacuolar pH used in the formation of blue flowers
Disclosure; Page 42-44; 62pp; English.
The V26 strain of Petunia was used. Poly A RNA was isolated from total RNA from flower buds and used to generate a cDNA library in Salmonella; T 6 R62757 standard; Protein; 192 Sequence Nijjar CS, Ralston EJ; Chuck GS, Vacuolar pH; Petunia Ph6 gene product. R62656; 26-APR-1993; US-054452. WO9425598-A. Salmonella SefU2 sequence. R62757; patterning in Drosophial. In plants, the motif is found in R(S) muscle development, and regulators of segmentation and organ sequence KKVQDLE (ending at residue 245). Proteins including this the sequence NHVLAER (starting at residue 192) and extending to the sequence comprises a helix-loop-helix structural motif starting with cDNA), the sequence for which is claimed (see Q73000 FT). The AA the left hand side of Ac was used to isolate pPet14-1 (contg. pH6the vector lambda ZapII (Stratagene). The SstI to BamHI fragment at N-PSDB; Q73000. WPI; 94-341349/42. 27-OCT-1994. WO9423561-A. /note= "see also 239..245" /label= Helix-loop-helix structural motif Region Petunia hybrida strain V26. 08-JUN-1995 26-APR-1994; IB0207 10-NOV-1994. 26-JUN-1995 (first entry) identity was found. Sequence 383 AA; (DNAP ) DNA PLANT TECHNOLOGY CORP. l6-APR-1993; US-049282. 15-APR-1994; U04173. (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J. 216 QLDREHLLSLEQRVVELQQTLAQKD 236 ql-rkkvqdlearanqteatlqtkd 259 158 YRAPCCESQEELALQHLVKEKLLAQ-LEEKLRVFANIVAVLNKEVEASHLALAASIH-QS 215 178 frkgcsitgeepsgnhvlaerrrreklnerfiilrslvpfvtk-mdkasi-lgdtieyvk 235 include the myc family of oncogenes, regulators of neuron and 23; Courtney-gutterson N, Dooner HK, SefU2; vaccine Conservative pH gene; Petunia. (first entry) Location/Qualifiers Score 105; DB 12; I Pred. No. 5.43e+00; 25; Mismatches 32; 8 240 == == == == Keller Length 383; :: :: <del>::</del> Indels 5**;** Gaps 5;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.5%;
Best Local Similarity 20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                               N-PSDB; Q27387.
Major Yo para-neoplastic antigenic polypeptide and its nucleic acid - for treatment and diagnosis of para-neoplastic cerebell:
                                                                               This sequence represents the major Yo paraneoplastic antigen polypeptide, and was deduced from the cDNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        paraneoplastic cerebellar degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R30429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R30429 standard; Protein; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The isolated SefU2 protein may be used in a vaccine composition to elicit an immune response to Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fimbrial type proteins.
Disclosure; Fig3A-3B; 95pp; English.
                                    cerebellar degeneration (PCD). Labelled antibodies to Yo can be used
                                                                                                                Claim 5; Fig 7; 57pp; English.
                                                                                                                                                                                                WPI; 92-284676/34.
                                                                                                                                                                                                                 Furneaux HM, Posner JB;
                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                            Misc_difference 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour cancer; brain; therapeutic agent; imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Major Yo paraneoplastic antigen (CDR62) encoded by clones pY1 pY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in animals (e.g. food producing animals) and humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella strains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eliciting an immune response to Salmonella - using attenuated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; Q73062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clouthier SC, Coli
WPI; 94-358275/44.
When coupled to a therapeutic agent, these Abs can be used to
                to determine whether a patient is carrying a tumour expressing Yo.
                                                detected using labelled Yo to see if a patient has paraneoplastic
                                                                  operlapping clones pY2 (Q27387) and pY1. Anti-Yo antibodies may be
                                                                                                                                                                                                                                                                                06-AUG-1992.
                                                                                                                                                                                                                                                                                                  WO9213093-A
                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "leucine zipper"
Domain 122..170
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-1993
                                                                                                                                                                                                                                (SLOK ) SLOAN KETTERING
                                                                                                                                                                                                                                                25-JAN-1991; US-646292.
                                                                                                                                                                                                                                                               24-JAN-1992; U00620
                                                                                                                                                                                                                                                                                                                             /note= "putative zinc finger"
Domain 52..80
                                                                                                                                                                                                                                                                                                                                                                          /note= "SPKK site"
                                                                                                                                                                                                                                                                                                                                                                                                        /note= ""super" leucine zipper"
                                                                                                                                                                                                                                                                                                            'note= "highly acidic (pI=3.4) activating domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 TKRCHESVCGRTVSLFSPAFYTAKYGYKL-C 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 SIHQSQLDR-EHLLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFLWKITNV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 skqqnqlsssereqemsaeivrlkrqlaerdeeltilqngldilretp-emkyvfiekhq 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aefsikaic-rvlqvarnswyvrrqqfrlvc 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collinson
                                                                                                                                                                                                                                                                                                                                                           205..231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector constructs, or compsns. contg.
                                                                                                                                                                                                                                INST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 103; DB 12;
Pred. No. 7.45e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                para-neoplastic cerebellar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCD; neurological symptoms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.5%;
Best Local Similarity 26.1%;
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R32698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSP polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete register with that at 171-192. However the characteristic basic DNA binding domain found in many leucine zipper proteins. There are also two other putative DNA binding motifs - a SPKK site at 201 and a zinc finger at 205-231, adjacent to the leucine
                                                                                Sequence
                                                                                                   The DNA encoding the heptad may be used to transform plants to increase the content of partic, amino acids such as lysine or methionine in seeds or leaves. See also See also R31979-86 and R32659-705.
                                                                                                                                                                                    expressed in vivo in plants to serve as a synthetic seed storage
                                                                                                                                                                                                                                                                                                                                  Falco SC, Keeler WPI; 93-076517/09.
                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-1991; US-743006.
                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1992; U06412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heptad;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R32698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activating domain between residues 52 and 80. The leucine zipper was found to have an unusual almost perfect homology with that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at residues 171-192. In addition allowing the substitution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     also a leucine zipper motif, distinctive of DNA binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secondary structure analysis of this sequence reveals a highly hydrophilic protein with extensive regions of alpha helix. There
                                                                                                                                                                 protein which can be custom-tailored for specific end-user requirements.
                                                                                                                                                                                                       The sequence represents a synthetic heptad polypeptide which can
                                                                                                                                                                                                                            Disclosure; Page 130; 176pp; English.
                                                                                                                                                                                                                                                   proteins with specified aminoacid content
                                                                                                                                                                                                                                                                     expressed in vivo in plants to serve as custom-tailored storage
                                                                                                                                                                                                                                                                                          Synthetic polypeptide(s) contg. specified heptad units
                                                                                                                                                                                                                                                                                                               N-PSDB; Q37279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9303160-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription factor is the presence of a highly acidic (pI=3.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zipper. Also consistent with the proteins function as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ser164 and His137 a "super" leucine zipper stretches from 122-170 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and when coupled to an imaging agent to locate neoplastic cells.
                                                                                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibit proliferation of neoplastic cells in a patient with PCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found in C-Fos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 VFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQ-KDQV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 vyeql-dvtareleetnqklvadskasq-qk--ilsltetieclqtnidhlqsqv 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 LERNIS-ELQI-QAAVEATGDLEVDCYRAPCCESQEEL-ALQHLVKE-KLLAQI-EEKIR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 lqqdlqlaaelgktlldrntele-dsvqqmyttnqeqlqeieyltkqvellrqmneqhak 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plants;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ა
•
                                                                              77 AA;
                                                                                                                                                                                                                                                                                                                                                     Keeler SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 custom tailored storage proteins; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      produced from clone 2-9.
                     24.3%;
                                                                                                                                                                                                                                                                                                                                                         Rice
Pred.
22; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 103; DB 5;
Pred. No. 7.45e+00;
                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
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                   99; DB 6; L
No. 1.39e+01;
                                        Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 509;
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Matches

18;

Conservative

Mismatches

32;

Indels

2; Gaps

2

S

183

:: ::

LEEKLRVFANIVAVINKEVEASHLALAASIHQ-SQLDREHLLSLEQRVVELQQTLAQKDQ 241

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US-08-446-915-2<sub>Tag</sub>

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RESULT
ID R7
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                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
/label=
                                            Lysine-rich synthetic storage protein SSP 7.7.7.7.7.8.9.8.9.5. (R18258) comprises 6 heptad SSP7 repeats (see R78237) followed by alternating SSP8 (R78245) and SSP9 (R78246) and SSP9 (R78246) and SSP5 heptads and a C-terminal SSP5 heptad (R78236) derived from vector pSK6. The SS was obtd. by insertion of SSP8 9.8.9-encoding oligonucleotides (Q95002-03) into the Earl site of clone 82-4 (Q94992) and use of
                                                                                                                                                                                                                                                                                                   Peptide
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1996 (first entry)
SSP 7.7.7.7.7.8.9.8.9.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R78258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R78258 standard; Protein; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soybean; Glycine max; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dihydrodipicolinic acid synthase; corn;
           be expressed in the seeds of transformed plants to increase the
                                                                                                                                               chloroplast transport sequence and seed specific promoter, also new
                                                                                                                                                                                                            Falco SC,
                                                                                                                                                                                                                                                 21-NOV-1994; U13190.
30-NOV-1993; US-1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lysine; synthetic storage protein; SSP; vector; pSK6;
                        clone 2-9 (Q95004).
                                                                                                                       Example 8;
                                                                                                                                   plants of improved nutritional value.
                                                                                                                                                                     New chimeric gene providing increased lysine content in plant seeds
                                                                                                                                                                                    N-PSDB; Q95004.
                                                                                                                                                                                                                                    30-NOV-1993; US-160117.
17-JUN-1994; US-261661.
                                                                                                                                                                                                                                                                          08-JUN-1995
                                                                                                                                                                                                                                                                                       W09515392-A1
                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1996
lysine content
                                 the resulting vector to transform Escherichia coli JM103, yielding
                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                      eptide
                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                   label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 VLGKLEHSLRIMEE 255
                                                                                                                                                          contains di:hydro:di:picolinic acid synthase gene coupled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                95-215272/28.
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                                                                                                                                                                                                                                                                                                   SSP5
                                                                                                                                                                                                                                                                                                                           SSP9
                                                                                                                                                                                                                                                                                                                                                    SSP8
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                                                                                                                      Page 145; 180pp; English
                                                                                                                                                                                                          Keeler SJ,
                                                                                                                                                                                                                                                                                                                                                                                      50..56
                                                                                                                                                                                                                                                                                                                                                                57..63
                                                                                                                                                                                                                                                                                                                                                                                                                                       35..42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22..28
                                                                                                                                                                                                                                                                                                               77
                       The SSP forms a coiled-coil structure.
                                                                                                                                                                                                            Rice
                                                                                                                                                                                                            JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  essential amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maize; Zea mays;
                                                                       SSP
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DE DE

Ethylene response (ETR) mutant protein etr1-2.

20-MAR-1996 (first entry)

R69851;

standard; Protein; 738

A

#### RESULT ID R2 Ş Ş В Ş 망 В 밁 Š Query Match Best Local S Matches Matches Best Local Similarity 24.3%; Query Match R26173 R26173; WPI; 92-284676/34. N-PSDB; Q27387. and when coupled to an imaging agent to locate neoplastic cells Sequence $430~\mathrm{AA}_{7}$ When coupled to a therapeutic agent, these Abs can be used to inhibit proliferation of neoplastic cells in a patient with PC detected using labelled Yo to see if a patient has paraneoplastic cerebellar degeneration (PCD). Labelled antibodies to Yo can be used Part of Major Yo paraneoplastic antigen (CDR62) encoded by clone pY paraneoplastic cerebellar degeneration; PCD; neurological symptoms; Sequence to determine whether a patient is carrying a tumour expressing Yo. clone pY2 as detailed in Q27387. Anti-Yo antibodies may be This sequence represents part of the major Yo paraneoplastic antigen polypeptide, and was deduced from the cDNA sequence of Claim 5; Fig 7; 57pp; English. degeneration acid - for treatment and Major Yo para-neoplastic Furneaux HM, Posner JB; 24-JAN-1992; U00620. 25-JAN-1991; US-646292. 06-AUG-1992. W09213093-A. Homo sapiens. tumour cancer; 27-JAN-1993 (SLOK ) SLOAN KETTERING 183 LEEKLRVFANTVAVINKEVEASHLALAASTHQ-SQLDREHLLSLEQRVVELQQTLAQKDQ 241 187 LRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQ-KDQV 130 242 VLGKLEHSLRLMEE 60 klkkmeeklkwmee 58 akvyeql-dvtareleetnqklvadskasq-qk--ilsltetieclqtnidhlqsqv 110 Local Similarity mes 31; Conser 1 meeklkameeklkameeklkameeklkame-eklkameeklkkmeeklkwmee 1 spqdlqla-aelg-ktlldrntele-dsvqqmyttnqeqlqeieyltkqvellrqmneqh 57 APMALERNISELQLQAAVEATGDIEVDCYRAPCCESQEEL-ALQHIVKE-KILAQI-EEK 186 standard; Protein; 430 18; 77 3.4%; ilarity 26.5%; Conservative Conservative (first entry) A brain; therapeutic agent; imaging; ss. --:: 255 73 INST CANCER antigenic polypeptide and its nucleic diagnosis of para-neoplastic cerebellar Score 101; DB 5; I Pred. No. 1.02e+01; 29; Mismatches 46; Pred. Score 22; Mismatches Ä e 99; DB 16; . No. 1.39e+01; 46; 32; Length 430; Length Indels Indels 11; 2; PCD ef. Gaps Gaps 59 10; 2

US-08-446-915-2.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.4%;
Best Local Similarity 26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
            etr1-3 and etr1-4 respectively. The cDNA sequences which encode these proteins can be linked to a promoter and used to transform plant cells of fruit bearing plants (in partic, the fruit is a
                                                                                                                                                                                                                                                                                                                                                         Ethylene response (ETR) mutant protein etr1-3. Ethylene response; recombinant; mutation; decrease; fruit ripening; abscission; floral senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R69852 standard; Protein; 738 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thaliana mutated ethylene response (ETR) proteins etr1-1, etr1-2, etr1-3 and etr1-4 respectively. The cDNA sequences which encode these proteins can be linked to a promoter and used to transform plant cells of fruit bearing plants (in partic. the fruit is a tomato) resulting in a decrease in response to ethylene. This enables controlled fruit ripening and delayed floral senescence and
                                                                                      Claim 2; Page 76-80; 212pp; English. R69850-R69853 represent the amino acid sequences of the Arabidopsis
                                                                                                                                                                                                                                             30-JUN-1994; U07418.
01-JUL-1993; US-086555.
28-JUN-1994; US-263480.
                                                                                                                                                                                                                                                                                                                                                                                                                                        R69852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bleecker AB, Chang C,
                                                                                                                                                                      N-PSDB; Q85560.
                                                                                                                                                                                          WPI; 95-061003/08.
                                                                                                                                                                                                            Bleecker AB,
                                                                                                                                                                                                                                                                                                                        WO9501439-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 71-74; 212pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transformed plants with decrease in response to ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q85559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 95-061003/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1994; U07418.
01-JUL-1993; US-086555.
28-JUN-1994; US-263480.
                                                                   thaliana mutated ethylene response (ETR) proteins etr1-1, etr1-2,
                                                                                                                                 transformed plants with decrease in response to ethylene
                                                                                                                                                   Modified ethylene response (ETR) nucleic acid - useful for producing
                                                                                                                                                                                                      (CALY ) CALIFORNIA INST OF TECHN.
Bleecker AB, Chang C, Meyerowit:
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R69850-R69853 represent the amino acid sequences of the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified ethylene response (ETR) nucleic acid - useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
WO9501439-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ethylene response; recombinant; mutation; decrease; fruit ripening;
   comato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 dllmeqnvaldlarreaetairarndflavmnhemrtpmhaiialssllqeteltpeqrl 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abscission during growth, transport or storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CALY ) CALIFORNIA INST OF TECHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JAN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abscission; floral senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 SLEQ--RVVELQQTLAQKDQVLGKLEH-SLRLMEEASFD-GTFLWKITNVTK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 mvetilkssnllatlmndvldlsrledgslql-elgtfnlhtlfrevlnlik 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resulting in a decrease in response to ethylene. This enables
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                          Meyerowitz EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meyerowitz EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 15;
Pred. No. 1.02e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Mismatches 37; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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abscission during growth, transport or storage. Sequence 738 AA;  Y. Match  Local Similarity 26.8%; Pred. No. 1.02e+01; ches 30; Conservative 36; Mismatches 37; I  21 dllmeqnvaldlarreaetairarndflavmnhemrtpmhaiials   ::     :   :    :    :     168 ELALQHLYKEKILAQLEEK-LRVFANIVAVLKKEVEAS-HLAIA  381 mvetilkssnllatlmndvldisrledgslql-elgtfnlhtlfre :    :            :     18 195 standard; Protein; 738 AA.  R69853; Standard; Protein; 738 AA.  R69853; Lindard; Protein; 738 AA.  R69853; Lindard; Protein; 738 AA.  R69853; Lindard; Protein; 738 AA.  R69853; US-086555.  Ethylene response (ETR) mutant protein etr1-4.  Ethylene response; recombinant; mutation; decrease; abscission; floral senescence.  N69901439-A2.  L1-JAA-1995.  30-JUN-1994; US-263480.  (CALY) CALIFORNIA INST OF TECHN.  Bleecker AB, Chang C, Meyerowitz EM; WPI; 95-061003/08.  N-PSDB; Q85561.  Modified ethylene response (ETR) nucleic acid - use transformed plants with decrease in response to eth Claim 2; Page 82-86; 212pp; English.  R69850-R69853 represent the amino acid sequences of thaliana mutated ethylene response (ETR) proteins e etr1-3 and etr1-4 respocitively. The cDMs sequences these proteins can be linked to a promoter and used plant cells of fruit bearing plants (in partic. the tomato) resulting in a decrease in response to ethylenchalses can be linked to a promoter and used plant cells of fruit bearing plants (in partic. the tomato) resulting in a decrease in response to ethylenchalses can be linked to a promoter and used plant cells of fruit bearing plants (in partic. the tomato) resulting in a decrease in response to ethylenchalses on the sequence of 738 AA;  248. Score 101. DB 15. 1-10.  248. Score 101. DB 15. 1-10.  249. Score 101. DB 15. 1-10.  240. Score 101. DB 15. 1-10.  24
abscission during growth, transport or storage. Sequence 738 AA; Sequence 738 AA; 1 Local Similarity 26.8%; Pred. No. 1.02e01; ches 30; Conservative 36; Mismatches 37; Indels 9; Gaps 321 dllmeqnvaldarreaetairarndflavmnhemtmhaiialssllqeteltpeqr1 380; :  ::

RESULT
ID R6
AC R6
DT 20

LT 14 R69849 standard; Protein; 738 R69849; 20-MAR-1996 (first entry)

A

US-08-446-915-2.mg

S ₽ Query Match 3.4%; Best Local Similarity 26.8%; Matches ethylene response (ETR) gene which codes for the ethylene response protein (R69849). The ETR cDNA or the full gene sequence (Q85556) can be mutated and linked to a promoter and used to transform plant cells of fruit bearing plants (in partic. the fruit is a tomato) resulting in a decrease in response to ethylene. This enables controlled fruit ripening and delayed floral senescence and N-PSDB; Q85557 Bleecker AB, Chang C, Q85557 represents the cDNA sequence of the Arabidopsis thaliana Claim 1; Page 59-62; 212pp; English. Modified ethylene response (ETR) nucleic acid - useful for producing WPI; 95-061003/08. Ethylene response (ETR) gene product. transformed plants with decrease in response to ethylene 01-JUL-1993; US-086555. 28-JUN-1994; US-263480. WO9501439-A2. Arabidopsis thaliana. Ethylene response; recombinant; mutation; decrease; fruit ripening; abscission during growth, transport or storage. 321 dllmeqnvaldlarreaetairarndflavmnhemrtpmhaiialssllqeteltpeqrl 380 (CALY ) CALIFORNIA INST OF TECHN. 30-JUN-1994; U07418. 2-JAN-1995. abscission; floral senescence. 168 ELALQHLVKEKLLAQLEEK-LRVFANIVAVLNKEVEAS-H--LALAASIHQSQLDREHLL 223 30; 738 AA; Conservative Meyerowitz EM; Score 101; DB 17, Pred. No. 1.02e+01; Length 738; Indels 9 Gaps ٦,

transformed plants with decrease in response to ethylene Claim 2; Page 65-68; 212pp; English. R69850-R69853 represent the amino acid sequences of the Arabidopsis Ethylene response (ETR) mutant protein etr1-1. Ethylene response; recombinant; mutation; decrease; fruit ripening; R69850; R69850 standard; Protein; 738 AA. Modified ethylene response (ETR) nucleic acid - useful for producing N-PSDB; Q85558. WPI; 95-061003/08. Bleecker AB, WO9501439-A2. Arabidopsis thaliana. 28-JUN-1994; US-263480. 01-JUL-1993; 30-JUN-1994; U07418 abscission; floral senescence. 20-MAR-1996 (first entry) (CALY ) CALIFORNIA INST OF TECHN. 2-JAN-1995 US-086555. Chang C, Meyerowitz EM;

these proteins can be linked to a promoter and used to transform plant cells of fruit bearing plants (in partic. the fruit is a thaliana mutated ethylene response (ETR) proteins etri-1, etri-2, etri-3 and etri-4 respectively. The cDNA sequences which encode S ₽

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tomato) resulting in a decrease in response to ethylene. This enables

controlled fruit ripening and delayed floral senescence and

ន្តន្តន abscission during growth, transport or storage. Sequence 738 AA;

Best Local Similarity 26.8%;
Matches 30; Conservative 36; Score 101; DB 15; Pred. No. 1.02e+01; Mismatches Length 738; Indels 9; Gaps

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Ş 밁 168 321 dllmeqnvaldlarreaetairarndflavmnhemrtpmhaiialssllqeteltpeqrl 380 :: = :: ::

밁 381 mvetilkssnllatlmndvldlsrledgslql-elgtfnlhtlfrevlnlik 431

224 SLEQ--RVVELQQTLAQKDQVLGKLEH-SLRLMEEASFD-GTFLWKITNVTK 271

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Search completed: Tue Dec 10 07:06:11 1996 Job time : 91 secs.